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Retinal phospholipase C from squid is a regulator of Gqa GTPase activity

Linnia H. Mayeenuddin, Christine Bamsey and Jane Mitchell

Department of Pharmacology, University of Toronto, Toronto, Ontario, Canada

Abstract

The phospholipase C (PLC) pathway is the major signaling mechanism of photoactivation in invertebrate photoreceptors. Here we report the cloning of a cDNA encoding a 140-kDa retinal PLC that is uniquely expressed in squid photoreceptors. This cDNA encodes a protein with multiple distinct modular domains: PH, X and Y catalytic, and C2 domains, as well as G- and P-box motifs and two GTP/ATP binding motifs. The PLC was stimulated by activated squid Gqa but not by squid Gqbg or mammalian bg subunits. The PLC was inhibited by monophosphate, diphosphate and triphosphate nucleotides but not cyclic nucleosides. We also tested the

ability of PLC-140 to regulate the GTPase activity of Gqa in the rhabdomeric membranes. Depletion of PLC-140 from the rhabdomeric membranes decreased the GTP hydrolysis but not GTPgS binding to the membranes. Reconstitution of purified PLC-140 with membranes accelerated Gqa GTPase activity by 8-fold at a concentration of 2.5 nM, suggesting that PLC-140 plays an important role in both the activation and inactivation pathways of invertebrate visual transduction.

Keywords: Gqa, GTPase, phospholipase C, photoreceptor, squid.

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The phosphoinositide-specific phospholipase C (PLC) enzymes are a family of proteins that hydrolyze membrane phosphoinositol-4,5 bisphosphate, to generate the second messengers inositol-1,4,5-trisphosphate (IP3) and diacylglycerol (DAG). PLC proteins are found in both vertebrate and invertebrate species as well as in yeast, slime molds,

species including: *Musca* (DeVary et al. 1987), *Limulus* (Fein 1986), and *squid* (Mitchell et al. 1995; Suzuki et al. 1995). Several invertebrate PLCs have been cloned and include two PLC isoforms from *Drosophila melanogaster* PLC-norpA and PLC-p21 (Bloomquist et al. 1988; Shortridge et al. 1991), and one from *lobster* (Xu and

fungi and plants (Rebecchi and Pentyala 2000). Thus far, 11 mammalian PLCs have been identified and they have been classified into four distinct groups: PLC-*b*, PLC-*g*, PLC-*d* and PLC-*l*. Of these four classes, the PLC-*b* and PLC-*l* isozymes demonstrate G protein-regulated activity. The PLC-*b* type enzymes are regulated by G protein *a* subunits of the G_q family (Kozasa et al. 1993; Lee and Rhee 1995; Biddlecome et al. 1996), as well as by G protein *bg* subunits (Waldo et al. 1991; Park et al. 1993a; Wu et al. 1993b) while PLC-*l* is regulated by monomeric Ras (Kelley et al. 2001)

The PLC pathway is the major signaling pathway in invertebrate photoreceptors. The molecular mechanism entails the photoactivation of rhodopsin leading to the stimulation of invertebrate G_q, which in turn activates retinal PLC. The role of G protein-regulated PLC activity in vision has been studied most extensively in photoreceptors of *Drosophila* (Bloomquist et al. 1988; Running Deer et al. 1995), but have also been reported in other invertebrate

McClintock 1999). A cDNA encoding a truncated PLC enzyme was also isolated from squid (Carne et al. 1999). We have previously reported the isolation and purification of a 140-kDa PLC protein from squid photoreceptors and shown it to be regulated by G_{qa} (Mitchell et al. 1995). We report the cloning of the full-length cDNA encoding 140-kDa PLC protein and demonstrate its regulation by protein subunits and nucleotides as well as its ability to regulate the GTPase activity of invertebrate G_{qa}.

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Address correspondence and reprint requests to J. Mitchell, Department of Pharmacology, Room 4342, University of Toronto, 1 King's College Circle, Toronto, Ontario, Canada M5S 1A8.
E-mail: jane.mitchell@utoronto.ca

Abbreviations used: DAG, diacylglycerol; IP₃, inositol-1,4,5-trisphosphate; PLC, phospholipase C.

Materials and methods

Cloning of squid phospholipase C

Oligonucleotide primers were designed based on previously published peptide sequences derived from a purified 140-kDa PLC protein (Mitchell et al. 1995). PCR reactions were performed using a squid retinal cDNA library as template (a generous gift from Drs J. K. Northup and M. Brownstein of NIH, Bethesda, MD, USA). A 472 base pair PCR product was generated that showed high sequence similarity to a truncated squid PLC (Carne et al. 1995) and primers based on the sequence from this truncated PLC produced a fragment of approximately 2600 base pairs. Further sequence information on the 3' end of the PLC cDNA was obtained using primers based on peptide four from purified PLC-140, and RACE (Sambrook and Russell 2001) reactions were performed to obtain the 5' and 3' UTRs using the gene-specific primers GCCTTAAATCAAACAAAGCTTATACCAAATTAT; TCC-AGTACAAGAAATATCCCTGGATCAA and the vector-specific primers TAATACGACTCACTATAGGGAGACCGGAAG; AAGGTTCTTCACAAAGATCCTTAGAGTC. Nucleotide sequences were determined for both strands of several positive clones

nitrocellulose membranes and immunoblotted with a polyclonal antibody raised against purified endogenous squid PLC-140 (Towbin et al. 1979).

Rhabdomeric membrane and purified protein preparations Photoreceptor membranes were prepared from frozen eyes taken from freshly caught *Loligo pealei* obtained from the Marine Biology Institute (Woods Hole, MA, USA) as previously described (Mitchell et al. 1995). The concentration of G_{qa} in the membranes was determined by quantitative immunoblotting using an antibody raised against the C-terminal sequence of G_{qa} (Upstate Biotechnology, Lake Placid, NY, USA) using recombinant squid G_{qa} as standard as previously described (Mitchell and Bansal 1997). PLC-140, G_{qa} and G_{bg} were purified from squid eyes as previously described (Mitchell et al. 1995; Bamsey et al. 2000).

Mammalian G_{bg} was purified from bovine ROS as described (Fung et al. 1992). Purified proteins were assessed by Coomassie blue staining following SDS-PAGE and determined to be ~90% homogeneous.

GTP_gS binding, GTPase and phospholipase C assays GTP_gS binding to rhabdomeric membrane preparations was

from each PCR reaction by automated DNA sequencing at a local facility. The full-length sequence obtained (GenBank accession number AF258528) was compared with DNA sequences in GenBank. Simple Modular Architecture Research Tool (SMART) was used to determine the domain topology of the protein encoded by the cDNA (Schultz et al. 2000) and PROSITE database search (Hofmann et al. 1999) was used to identify biologically significant sites encoded by the cDNA. PEST and program (Rogers et al. 1986; Rechsteiner and Rogers 1996) was used to identify PEST sequences in PLC-140.

Expression of recombinant PLC-140 in *Escherichia coli*
 The protein encoded by the PLC-140 cDNA was expressed in BL21-SI cells using Gibco BRL Gateway Cloning Technology (Gibco-BRL, Gaithersburg, MD, USA). The full-length coding region of PLC-140 cDNA was PCR amplified using Clontech Advantage HF-2 PCR kit (Clontech Laboratories, Palo Alto, CA, USA) with attB1-FS and attB2-FA primers. Entry clones were generated in DH5a cells using the full-length attB PCR product and attP containing pDONR201 vector. Plasmid DNA from positive entry clones were isolated and used to generate His-tagged expression clones in pDEST17 vectors.

Bacterial BL21-SI colonies expressing His-tagged PLC-140 were induced with 0.3 mM NaCl. PLC-140 protein expression was analyzed via western blotting using antiserum raised against purified PLC-140. Recombinant PLC-140 (rPLC-140) protein was purified from bacterial extracts under denaturing conditions (8.0 M urea, 10 mM Tris pH 8.0, 100 mM NaH₂O₂, 500 mM NaCl) with Ni-NTA resin (Qiagen, Valencia, CA, USA) with slight modifications to manufacturer's instructions. The resin was washed in buffer containing 6 M urea, 20 mM Tris pH 8.0, 500 mM NaCl, 50 mM imidazole, and the proteins renatured using a stepwise gradient from 6 to 0 M urea in 20 mM Tris pH 8.0, 500 mM NaCl in 0.5 M increments prior to elution. The semipurified recombinant PLC protein (PLC was assessed as approximately 50% of the protein content of eluted fractions) was analyzed by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) on 8% polyacrylamide gels (Laemmli 1970), transferred to

determined by incubating 5 mg of membranes in 20 mM NaHEPES pH 7.5, 3 mM MgCl₂, 100 nM GTP_gS (50,000 cpm/pmol) at 22°C at times indicated in individual experiments, binding reactions were stopped by dilution with 2 mL of ice-cold stop buffer (20 mM NaHEPES pH 7.5, 3 mM MgCl₂), followed by rapid \otimes nitrocellulose filters. After washing filters three times in 3 mL of stop buffer the filters were dried and [³⁵S]GTP liquid scintillation counter.

GTPase activity was assessed in rhabdomeric membranes under conditions in which the GTP concentration is lower than that of G_qa by incubating 10 mg of membranes (containing 1.2 pmole G_qa) at 22°C in 20 mM NaHEPES pH 7.5, 3 mM MgCl₂ [g -³²P]GTP (50 000 cpm/pmol). GTP hydrolysis was initiated by the addition of membranes and purified endogenous PLC and stopped by addition of 100 mL of 6% perchloric acid. Nucleotides were removed by addition of 700 mL of 10% activated charcoal in 20 mM NaPO₄ buffer pH 7.5 and free [³²P] measured by scintillation counting.

Regulation of purified endogenous PLC-140 activity was measured by reconstituting aliquots of G_qa (1 ng), G_{qbg} (10 ng) or G_{tbq} (175 ng) with PLC-140 (2 ng) in the presence of [³²P]PIP₂/PE vesicles in the presence of 1 mM free Ca²⁺ volume of 50 mL as described previously (Mitchell et al. 1995; Bamsey et al. 2000).

Data presentation

are reported \pm SD, unless otherwise noted in the figure legends.

Results

Amino acid sequence, domain structure and tissue distribution of squid phospholipase C (PLC-140) The full-length cDNA encoding squid retinal PLC-140 had a 3381 nucleotide open reading frame. The deduced amino acid sequence derived from this cDNA is shown in Fig. 1(a) along with the sequence of the two other PLC isozymes

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Fig. 2 Expression of PLC-140 in native and recombinant systems.
 Samples of rhabdomeric membranes (Rhabs) or of washed rhabdomeric membranes (W-Rhabs) containing 1.6 pmoles G_{qa}, 0.08 mg of purified endogenous PLC-140 (nPLC-140), 1 mL of an extract from *E. coli* transformed with a cDNA encoding his-tagged PLC-140 (bExt) and 30 mL of the extract following purification over Ni-afinity column (rPLC-140), were subjected to western blot analysis with an antibody raised against purified PLC-140. Dashes on the right side of the figure indicate the migration of molecular weight standards from top: a γ -macroglobulin (180 000), b-galactosidase (116 000), fructose-6-phosphate kinase (84 000), pyruvate kinase (58 000), fumarase (48 500), lactic dehydrogenase (36 500) and triosephosphate isomerase (26 600).

expressed in retinal photoreceptors; mammalian PLC-b4 and *Drosophila* norpA. The four peptides derived from purified PLC-140 on which the oligonucleotide primers were based were all present within the cDNA. When transformed into *E. coli* the cDNA encoding PLC-140 produced a protein that was similar in size to the native PLC found in squid membranes as well as the PLC purified from these membranes. The recombinant protein was

Fig. 3 Tissue distribution of PLC-140. Homogenates prepared from various squid tissues (10 mg for retina and 30 mg for all other tissues) were subjected to SDS PAGE followed by western blot analysis with an antibody raised against purified PLC-140. Dashes on the right side of the figure indicate the migration of molecular weight standards from top: a γ -macroglobulin (180 000), b-galactosidase (116 000), fructose-6-phosphate kinase (84 000), pyruvate kinase (58 000), fumarase (48 500), and lactic dehydrogenase (36 500).

similarity was found as anticipated to the truncated northern European squid PLC (Carne et al. 1995). PLC-140 also had significant similarity with the two *Drosophila* PLCs: norpA and PLC-21 (37%), and a recently identified PLC from lobster (35%) (Xu and McClintock 1999). Identity of PLC-140 with the mammalian PLC isozymes of the b family ranged between 39 and 40% with PLC-b1 and b4, and 36±39% identity with PLC-b2 and b3.

The domain structure of PLC-140 as determined using SMART module was found to include six distinct domains: pleckstrin homology (PH), X and Y catalytic, C2, G- and P-boxes. There were also two ATP/GTP-binding site motifs

recognized by an antibody raised against purified PLC-140 as demonstrated by western blot analysis (Fig. 2).

Comparison of the deduced amino acid sequence of this PLC with other sequences in the database revealed the protein to be similar in structure and organization to other members of the PLC-*b* family of proteins. Highest sequence

identity was within the PLC sequence (Fig. 1b).

A survey of tissues taken from *Loligo pealei* by immunoblot using a polyclonal antibody raised against purified PLC-140 demonstrated expression of this protein only in the eye (Fig. 3). Neither the peripheral tissues nor the optic ganglion demonstrated any immune reactivity to

Fig. 1 (a) Alignment of the deduced amino acid sequence of squid PLC-140 (AF258528) with *Drosophila norpA* PLC (norpA: AF181641) and rat PLC-*b4* (A48047). The asterisks denote conserved amino acid residues in all the aligned sequences, the dots denote residues that are conserved in two or more proteins and the double dots denote conservative amino acid substitutions. The dashes represent gaps introduced for optimal alignment. (b) Domain structure of

PLC-140. It contains six distinct modular domains: pleckstrin homology domain (PH: 22±144), PLC catalytic domains (X: 323±471 and Y: 514±630) and calcium binding domain (C2: 651±750). P- and G-box motifs span amino acids 1016±1047 and 1069±1096, respectively. A putative PEST sequence region (score 1.3.26) designates the putative site of calpain cleavage (858±881) and * designates ATP/GTP binding site motifs (344±351 and 815±822).

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Table 1 | ³⁵ S]GTPgS binding to purified PLC-140

Additions	[³⁵ S]GTPgS
None	100 ± 9
GMP 1 μM	18 ± 3
GDP 1 μM	34 ± 12
GTP 1 μM	25 ± 4
GTPgS 1 μM	19 ± 5
cGMP 1 μM	137 ± 13
ATP 1 μM	43 ± 12
cAMP 1 μM	128 ± 15
Mg ²⁺ 10 μM	99 ± 4
Ca ²⁺ 1 μM	123 ± 14

A total of 2 ng of purified PLC-140 were incubated with 120,000 cpm [³⁵ S]GTPgS (923,000 cpm/pmol) for 30 min in the presence of the indicated compounds. Samples were quenched and [³⁵ S] protein determined as described in Materials and methods. Results are shown as percentage of [³⁵ S] bound to PLC-140 additional compounds (4.3 ± 0.4 fmoles GTPgS bound) and are the mean ± SD of triplicate determinations.

activity approximately 70% over basal activity. Addition of the same concentration of G_qa activated by AIF resulted

Fig. 4 Regulation of PLC-140 activity by G proteins and ribonucleotides. (a) Puri®ed endogenous PLC-140 (2 ng) was incubated with phospholipid vesicles containing PIP2 in the absence (control) or presence of 1 ng of Gqa, 1 m NaF, 2 m AlCl₃ (AlF control), 1 ng of activated Gq (Gqa-AlF), 10 ng of Gbg puri®ed from squid rhabdomeric membranes, or 175 ng of Gbg puri®ed from bovine ROS. (b) Puri®ed PLC-140 was assessed in the absence (control) or presence of the indicated compounds at a final concentration of 0.1 or 1 m as described under Materials and methods. The results are means ± SD of two experiments and are expressed as a percent of the activity in the absence of G protein subunits or nucleotides. The activity in control samples corresponding to 100% was 15 ± 2 pmol/min and 17 ± 3 pmol/min in experiments a and b, respectively.

the PLC antibody, indicating that the expression of this PLC protein is very specific to the squid photoreceptors.

Regulation of PLC-140 by Gqa, Gbg and nucleotides
The similarity in structure between PLC-140 and the other retinal PLC-b isozymes, norpA and PLC-b4, suggested that squid retinal PLC may show a similar pattern of regulation as these other proteins. We tested the effect of both squid and mammalian visual Gbg on endogenous puri®ed PLC-140 in reconstitution assays and compared this to the activation seen by Gqa subunits that we have reported previously. Addition of 0.45 nm Gqa stimulated the PLC

increased activation of PLC-140 to 10-fold stimulation the basal activity of PLC-140 in the presence of AlF alone (Fig. 4a). Addition of a molar excess of either squid 6 n Gbg or 100 nm mammalian retinal Gb increased the PLC activity. The presence of GTP/ATP binding in the PLC-140 sequence suggested that nucleotides may regulate its activity and this was demonstrated for both guanine and adenine nucleotides that were both found to inhibit PLC activity in a concentration-dependent manner (Fig. 4b). PLC-140 was able to bind [3H]GTP with stoichiometry of approximately 0.3 mole of GTPgS/mol PLC and this binding was inhibited by unlabeled guanine monophosphate, guanine diphosphate and guanine triphosphate as well as adenosine triphosphate; however, cyclic adenosine monophosphate or cyclic guanine monophosphate were not able to displace GTPgS. Binding of nucleotide to PLC-140 was unaffected by the presence of magnesium ions. PLC-140 was slightly enhanced in the presence of calcium (Table 1).

PLC regulation of Gqa GTPase activity

PLC-b1 has previously been demonstrated to increase the rate of GTP hydrolysis of mammalian Gqa (Chidiac and Ross 1999). Given the similarity between the squid Gqa protein and its mammalian counterparts of the Gq family (Ryba et al. 1993) we decided to test the effect of PLC-140 on the GTPase activity of squid Gqa. The squid Gq protein binds GTP very rapidly in the presence of light-activated rhodopsin but extremely slowly when removed from the rhabdomeric membranes, with rate constants for GTPgS

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Fig. 5 [³⁵S]GTP_S binding and GTPase activity of rhabdomeric and washed rhabdomeric membranes. (a) [³⁵S]GTP_S binding to rhabdomeric membranes (B) or washed-rhabdomeric membranes (O) containing 1.6 pmoles G_qa was assessed for 0±60 s as described under Materials and methods. Reactions were stopped and [³⁵S]GTP_S bound to membranes was counted and plotted as a function of time. (b) the G_qa GTPase activity of rhabdomeric and washed-rhabdomeric membranes was determined by incubating membranes with [³²P]GTP for 0±60 s as described under Materials and methods. Reactions were quenched and the supernatants counted and plotted as a function of time. All values are the averages of duplicate reactions from representative experiments.

binding of 7.7/min and 0.23/min, respectively (data not shown). PLC-140 and other loosely associated proteins could be removed from the squid rhabdomeric membranes by washing in buffers containing 0.5 M NaCl (Fig. 2, W-Rhabs). We found no change in the GTP_S binding to the membranes following this washing procedure (Fig. 5a); however, there was a significant decrease in the rate of GTP hydrolysis in the washed membranes compared with the original rhabdomeric membranes (Fig. 5b). Reconstitution of purified endogenous PLC-140 with the washed membranes increased the GTPase activity 20-fold (Fig. 6a). When the stimulation of G_q GTPase activity was measured over a range of PLC-140 concentrations in the assay it was found that a molar ratio of PLC-140 : G_qa of 2 : 1 was required in order to have any effect on GTPase activity.

Fig. 6 Regulation of G_qa GTPase activity by PLC-140. (a) The G_qa GTPase activity in washed-rhabdomeric membranes containing 2.5 pmoles G_qa was measured in the absence (B) or presence (O) of 20 pmoles of purified endogenous PLC-140 for 0±60 s as described under Materials and methods. [³²P]_i was counted and plotted as the percentage of the maximal GTP hydrolysis as a function of time. (b) The effect of PLC-140 on G_qa GTPase activity was measured in washed-rhabdomeric membranes. Increasing concentrations of purified PLC-140 were added to the membranes containing 2.5 pmoles G_qa and the GTPase reaction was initiated at time 0 by the addition of [³²P]GTP. Reactions were stopped after 10 s by the addition of perchloric acid and [³²P]_i counted and plotted as the percentage of maximal GTP hydrolysis. Data points are the means of duplicate samples and are representative of two separate experiments.

This GAP activity increased to a maximal effect seen with a 10±20-fold molar excess of PLC (Fig. 6b).

Discussion

A cDNA that encodes the PLC enzyme we have previously isolated from squid rhabdomeric membranes was isolated in this study. This PLC protein was only found in the squid eye and not identified in any other tissue from squid under the conditions that we have used in our study. PLC isozymes expressed in visual systems of other invertebrates have not been shown to have such specific tissue distribution. Lobster PLC-b was found to be widely expressed in many tissues (Xu and McClintock 1999) and *Drosophila norpA*, while predominantly expressed in the eye is also found in the optic

Fig. 7 The role of PLC-140 regulation in visual transduction in squid photoreceptors. The model presents the molecular components of the squid visual system. Rhodopsin activation by light regulates GDP-GTP exchange on G_{qa} facilitating the G_q activation of PLC-140. PLC activation increases the production of inositol 1,4,5-trisphosphate (IP₃) and diacylglycerol (DAG) from inositol bisphosphate. IP₃ stimulates the release of calcium from subrabdomeric stores and the combination of calcium and DAG may lead to the opening of ion channels and depolarization of the membrane. Two reactions that limit the activation of this system are shown. First, the PLC-140 interaction with G_{qa}-GTP increases the rate of GTP hydrolysis by the G_{qa} protein, limiting the time of PLC activation by the G_{qa} protein. Second, the increase in calcium concentration stimulates a phosphodiesterase (PDE) in the squid photoreceptor leading to an increase in nucleotide concentrations that are inhibitory to PLC-140 activity.

lobe and brain (Bloomquist et al. 1988). Further identification of the mRNA encoding the PLC enzyme and its expression in the various squid tissues is required to determine if the expression of the gene encoding PLC-140 is in fact eye-specific; however, the eye is clearly the site of highest expression of this protein.

The domain structure of PLC-140 was very similar to other PLC enzymes of the b family. As expected, the similarity between PLC-140 and other PLC-b enzymes is

and PLC-b2, and since we have shown that purified PLC-140 is activated by calcium and squid G_q, they may be sites for this regulation.

PLC-140 has a long carboxyl terminal region that contains the P-box and G-box motifs required for activation by G proteins (Lee et al. 1993; Park et al. 1993b; Wu et al. 1993a; Kim et al. 1996). The truncated squid PLC that we identified by Carne et al. (1995) lacked a carboxyl-terminal tail and does not encode P- or G-box motifs and may therefore not be sensitive to G_{qa}-dependent activation. In support of this notion, we have seen cleavage of purified PLC-140 by exogenous calpain with loss of G_{qa} regulation (L. H. Mayeenuddin, unpublished data). Although we have not been able to obtain amino acid sequence from calpain-digested PLC-140 fragments, cleavage of the protein in a region near the putative PEST sequence which spans amino acids 858±881, positive PEST score of 3.26 (Sekhar and Free 1998), would produce protein fragments of approximate size observed by us and others (Suzuki et al. 1999). Carboxyl-terminal truncations have also been reported for mammalian PLC-b1, PLC-b3 and PLC-b4 (Park et al. 1993b; Banno et al. 1995; Kim et al. 1998). The effect of these truncations on PLC activation is enzyme-specific. Cleavage of PLC-b3 by calpain renders the truncated PLC more sensitive to regulation by G protein bg subunits (Banno et al. 1995), while the C-terminally truncated sp variant of PLC-b4, PLC-b4b, has been shown to be insensitive to regulation by both G_{qa} and G_{bg} (Kim et al. 1998). The bg sensitivity of the calpain-digested PLC-140 has not been tested; however, given the lack of bg regulation of intact PLC-140 shown here, it seems unlikely that the truncated protein will be bg-sensitive.

Two ATP/GTP binding sites were identified within the deduced amino acid sequence of PLC-140. The GHOL TGKS sequence found within the X domain of PLC-140 (amino acids 344±351) and the AAKPVKGK sequence (amino acids 814±822) located between the C domain and the P- and G-boxes, both correspond to the (G/A)X4GK(S/T) identified as one of the motifs found in members of the GTPase superfamily (Bourne et al. 1993). These are similar to the motifs found within PLC-b4 and norpA also within the X domains of these PLC isozymes (Lee et al. 1993). We have shown here that PLC-140 is able to bind guanine and adenine monophosphorylated,

greatest within the conserved X and Y catalytic domains (65±70% identity). These two regions are highly conserved amongst all PLC isozymes and they are essential for catalytic activity (Bristol et al. 1988; Ellis et al. 1993). The PH and C2 domains of PLC-140 represent structurally conserved protein modules, which in other PLC-b enzymes have been shown to be involved in diverse calcium and lipid interactions (Rizo and Sudhof 1998; Kutan and Allen 1999). The PH and C2 domains of PLC-140 show 60±85% sequence similarity to the respective domains in PLC-b1

diphosphorylated and triphosphorylated nucleotides but cyclic nucleotides. Similar to PLC-b4 (Lee et al. 1994), guanine and adenine nucleotides inhibited the activity of PLC-140. It is possible that binding of nucleotides with the X domain could disrupt the catalytic activity of these enzymes.

The lack of PLC-140 regulation by G protein bg subunits and inhibition by ribonucleotides, distinguishes this enzymes as a member of an emerging subgroup of PLC-b proteins involved in visual systems. It has been

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speculated that inhibition of PLC-b4 by monophosphate, diphosphate and triphosphate but not the cyclic nucleotides may be a mechanism for their regulation in the mammalian photoreceptors where the concentrations of GMP, GTP and cGMP are of course regulated by light (Lee et al. 1994). In the invertebrate visual systems, the major light-stimulated transduction pathway does not involve regulation of nucleotide hydrolysis, nevertheless, there have been reports of effects of guanine nucleotides in Limulus (Johnson et al. 1986) and squid (Saibil 1984) as well as a report of calcium-stimulated cGMP phosphodiesterase activity in squid eyes (Brown and Kelman 1996). Possibly, in the invertebrate eye, light regulates nucleotide concentrations via a PLC-stimulated rise in intracellular calcium and subsequent activation of cyclic nucleotide hydrolysis. Such a scheme is outlined in Fig. 7, where the nucleotide suppression of PLC activity is proposed as a mechanism to limit the activity of the PLC in the face of rising calcium levels and reduce the gain of the invertebrate visual system that occurs downstream of the PLC. If this mechanism exists then one would anticipate that inhibition of phosphodiesterase activity would lead to an increase in both the amplitude and duration of responses to light. Indeed, these were the findings when the PDE inhibitor zaprinast was introduced into Limulus photoreceptors (Johnson and O'Day 1995). These authors found that the effect of zaprinast was only seen in response to stimulation by bright light, required calcium and was upstream of IP3 production. Clearly, there are alternative explanations for these observations and more

phospholipids and Gq protein a subunits, consistent with our observations of the regulation of purified PLC-140 protein. The demonstration that this protein can be inhibited by nucleotides and acts to limit the activity of its own stimulator, Gqa, suggests that PLC-140 plays a pivotal role in both the activation and inactivation of cephalopod visual systems.

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work is needed to test if regulation of PLC by nucleotides does exist in vivo in an invertebrate visual system.

We have also examined the effect of PLC-140 on G_{qa} activity by regulation of its GTPase activity. We first observed a change in GTPase activity of rhabdomeric membranes following removal of loosely associated proteins that include PLC-140. Reconstitution of purified PLC-140 back to these membranes in molar excess of G_{qa} increased the GTPase activity 2.5-fold. The requirement for an excess of PLC to G_{qa} in order to significantly influence the rate of inactivation of G_{qa} is in keeping with our estimates of a threefold molar excess of total PLC-140 to total G_{qa} in the whole squid eye. It is not difficult to envision that an even greater concentration of PLC could occur at specific sites within the microvillar structure in response to light stimulation. Recent studies in *Drosophila* have also shown dependence of GTPase activity of dG_q on the high concentrations of norp A PLC (Cook et al. 2000). It seems that feedback inhibition of invertebrate G_{qa} proteins by PLC is common to invertebrate visual systems and is required for single-photon responses in these systems.

In conclusion, we have cloned a cDNA encoding a PLC that appears to be the major effector of squid visual systems. This protein contains a number of identifiable domains that may be sites of interaction of PLC-140 with membranes,

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 NCBI results of BLAST

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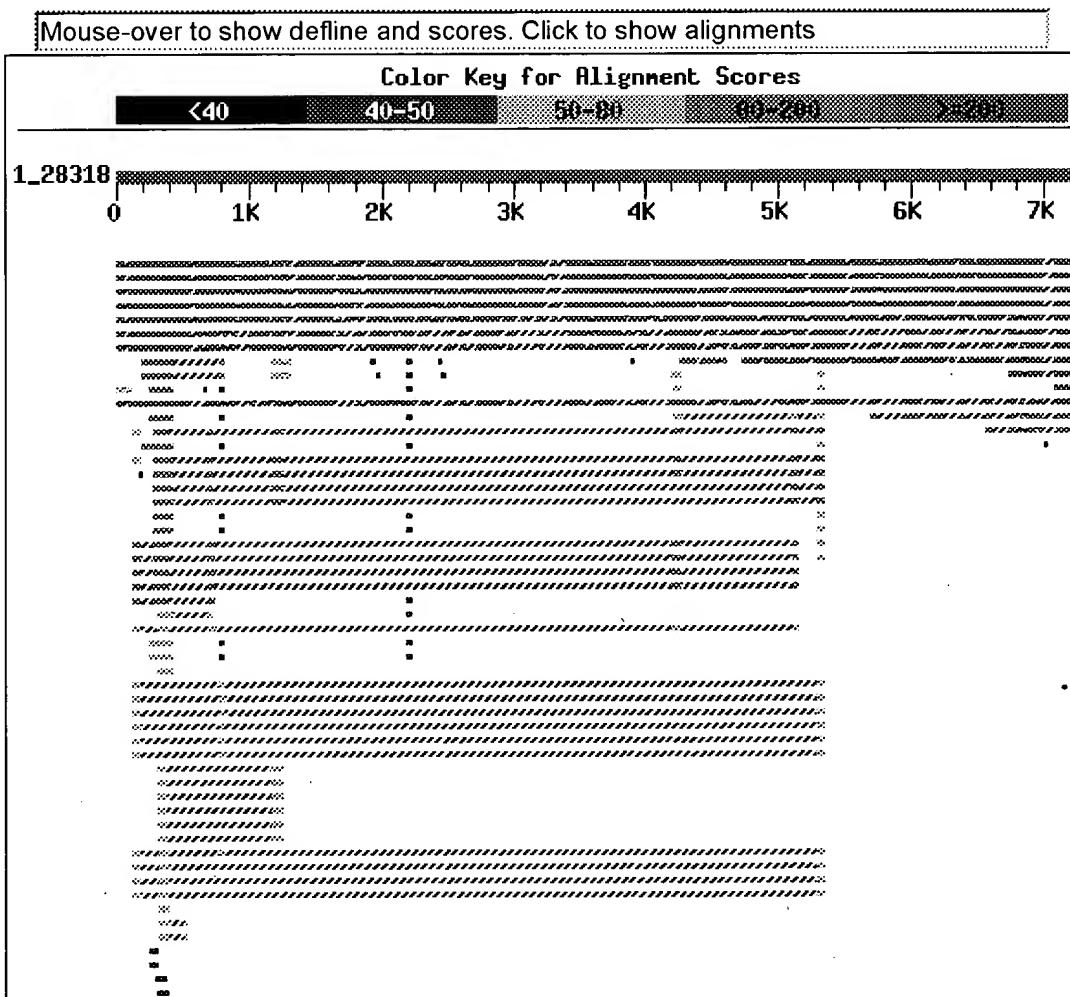
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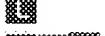
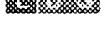
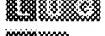
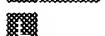
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

1,968,555 sequences; 9,458,193,315 total letters

Taxonomy reports**Distribution of 1012 Blast Hits on the Query Sequence**

Sequences producing significant alignments:

(bits) Value

gi 9507134 ref NM_019167.1	Rattus norvegicus beta-spectrin...	383	e-102	
gi 11066460 gb AF225960.1 AF225960	Rattus norvegicus spectr...	383	e-102	
gi 3550974 dbj AB008551.1	Rattus norvegicus mRNA for beta...	383	e-102	
gi 3452552 dbj AB001347.1	Rattus norvegicus Spnb-3 mRNA fo...	383	e-102	
gi 38084793 ref XM_129130.5	Mus musculus spectrin beta 3 (...)	343	3e-90	
gi 5902121 ref NM_006946.1	Homo sapiens spectrin, beta, no...	224	2e-54	
gi 29179634 gb BC048851.1	Mus musculus, Similar to beta-sp...	224	2e-54	
gi 23271110 gb BC033305.1	Mus musculus, clone IMAGE:401041...	224	2e-54	
gi 2511783 gb AF026489.1 AF026489	Mus musculus beta III spe...	224	2e-54	
gi 3550976 dbj AB008567.1	Homo sapiens mRNA for beta-spect...	224	2e-54	
gi 19879811 dbj AP001157.4	Homo sapiens genomic DNA, chrom...	208	1e-49	
gi 2511780 gb AF026488.1 AF026488	Homo sapiens beta III spe...	149	8e-32	
gi 2511778 gb AF026487.1 AF026487	Homo sapiens beta III spe...	149	8e-32	
gi 26090589 dbj AK044883.1	Mus musculus 9.5 days embryo pa...	133	5e-27	
gi 22507315 ref NM_000347.3	Homo sapiens spectrin, beta, e...	103	4e-18	
gi 24475587 ref NM_013675.2	Mus musculus spectrin beta 1 (...)	103	4e-18	
gi 440899 gb S66283.1 S66283	Spnb-1=beta-spectrin [mice, re...	103	4e-18	
gi 338439 gb J05500.1 HUMSPTB	Human beta-spectrin (SPTB) mR...	103	4e-18	
gi 34879631 ref XM_240072.2	Rattus norvegicus spectrin bet...	101	2e-17	
gi 34866099 ref XM_234322.2	Rattus norvegicus similar to S...	100	7e-17	
gi 7106420 ref NM_009260.1	Mus musculus spectrin beta 2 (S...	94	4e-15	
gi 30348965 ref NM_175836.1	Mus musculus spectrin beta 2 (...)	94	4e-15	
gi 26348244 dbj AK079842.1	Mus musculus 0 day neonate thym...	94	4e-15	
gi 598330 gb M74773.1 MUSSPNA	Mus musculus brain beta spect...	94	4e-15	
gi 4102882 gb AF017112.1 AF017112	Mus musculus non-erythroc...	94	4e-15	
gi 4102750 gb AF016040.1 AF016040	Mus musculus beta spectri...	94	4e-15	
gi 4507194 ref NM_003128.1	Homo sapiens spectrin, beta, no...	86	1e-12	
gi 30315657 ref NM_178313.1	Homo sapiens spectrin, beta, n...	86	1e-12	
gi 21327798 gb BC032061.1	Homo sapiens, clone IMAGE:517353...	86	1e-12	
gi 27462179 gb AF327441.1	Homo sapiens beta-spectrin 2 iso...	86	1e-12	
gi 338442 gb M96803.1 HUMSPTBN1A	Human general beta-spectri...	86	1e-12	
gi 425552 gb S65762.1 S65762	SPTBN1=beta-fodrin [human, mRN...	76	1e-09	
gi 22204389 emb AL672225.15	Mouse DNA sequence from clone ...	74	4e-09	
gi 1657656 gb U73171.1 MMU73171	Mus musculus brain beta-spe...	70	6e-08	
gi 18250160 gb AC093110.4	Homo sapiens BAC clone RP11-564H...	66	1e-06	
gi 13990322 emb AL121774.5 CNS01DSF	Human chromosome 14 DNA...	66	1e-06	
gi 14625740 emb AL135745.5 CNS01DVD	Human chromosome 14 DNA...	66	1e-06	
gi 392912 gb U00910.1 HSU00910	Human beta-spectrin (HSPTB1)...	66	1e-06	
gi 13435160 ref NM_025213.1	Homo sapiens spectrin, beta, n...	64	4e-06	
gi 24642831 ref NM_078664.2	Drosophila melanogaster beta S...	64	4e-06	
gi 21734932 gb AC020929.6	Homo sapiens chromosome 19 clone...	64	4e-06	
gi 22832735 gb AE003506.2	Drosophila melanogaster chromoso...	64	4e-06	
gi 11992161 gb AF311855.1 AF311855	Homo sapiens spectrin be...	64	4e-06	
gi 14028959 gb AC012161.8 AC012161	Drosophila melanogaster,...	64	4e-06	
gi 14028958 gb AC011703.8 AC011703	Drosophila melanogaster,...	64	4e-06	
gi 14028957 gb AC011702.10 AC011702	Drosophila melanogaster...	64	4e-06	

gi 3901275 gb AF079569.1 AF079569	Homo sapiens beta III spe...	64	4e-06	
gi 11602889 gb AY004227.1	Homo sapiens betaIV spectrin iso...	64	4e-06	
gi 11602886 gb AY004226.1	Homo sapiens betaIV spectrin iso...	64	4e-06	
gi 11602835 gb AF082075.1 AF082075	Homo sapiens beta4sigma1...	64	4e-06	
gi 157019 gb M92288.1 DROBSP	D.melanogaster beta-spectrin...	64	4e-06	
gi 31201698 ref XM_309797.1	Anopheles gambiae ENSANGP00000...	62	2e-05	
gi 31201696 ref XM_309796.1	Anopheles gambiae ENSANGP00000...	62	2e-05	
gi 34855388 ref XM_218364.2	Rattus norvegicus similar to b...	58	2e-04	
gi 30794219 ref NM_032610.1	Mus musculus spectrin beta 4 (...)	58	2e-04	
gi 20372321 gb AY032694.1 Y032691S04	Mus musculus beta-spec...	58	2e-04	
gi 16117404 gb AY032655.1	Mus musculus beta4-spectrin mRNA...	58	2e-04	
gi 18147601 dbj AB055618.1	Mus musculus mRNA for betaIV-sp...	58	2e-04	
gi 30160427 gb BC051562.1	Mus musculus cDNA clone IMAGE:15...	56	0.001	
gi 20372320 gb AY032693.1 Y032691S03	Mus musculus beta-spec...	56	0.001	
gi 22204468 emb AL731792.12	Mouse DNA sequence from clone ...	54	0.004	
gi 18859422 ref NM_131525.1	Danio rerio spectrin, beta, er...	50	0.058	
gi 20372340 gb AY032713.1 Y032691S23	Mus musculus beta-spec...	50	0.058	
gi 11992163 gb AF311856.1 AF311856	Homo sapiens spectrin be...	50	0.058	
gi 9944860 gb AF262336.1 AF262336	Danio rerio beta-spectrin...	50	0.058	
gi 6453546 emb AL133093.1 HSM801370	Homo sapiens mRNA; cDNA...	50	0.058	
gi 18147607 dbj AB055621.1	Mus musculus mRNA for betaIV-sp...	50	0.058	
gi 18147605 dbj AB055620.1	Mus musculus mRNA for betaIV-sp...	50	0.058	
gi 18147603 dbj AB055619.1	Mus musculus mRNA for betaIV-sp...	50	0.058	
gi 10047360 dbj AB046862.1	Homo sapiens mRNA for KIAA1642 ...	50	0.058	
gi 13540713 ref NM_022401.1	Rattus norvegicus plectin (Ple...	48	0.23	
gi 9581948 gb AC004965.2	Homo sapiens PAC clone RP5-1106H1...	48	0.23	
gi 1292885 emb X59601.1 RNPLECT	Rat mRNA for plectin	48	0.23	
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gi 19718730 ref NM_058243.1	Homo sapiens bromodomain conta...	46	0.90	
gi 7657217 ref NM_014299.1	Homo sapiens bromodomain contai...	46	0.90	
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gi 34304491 gb AY356552.1	Canis familiaris beta-spectrin m...	46	0.90	
gi 30984902 gb AC109322.16	Homo sapiens chromosome 8, clon...	46	0.90	
gi 2345059 gb AF013172.1 AH005869S01	Homo sapiens beta-spec...	46	0.90	
gi 23274170 gb BC035266.1	Homo sapiens, Similar to bromodo...	46	0.90	
gi 28839047 gb BC047888.1	Homo sapiens, Similar to bromodo...	46	0.90	
gi 28277311 gb BC046267.1	Xenopus laevis, Similar to spect...	46	0.90	
gi 27804345 gb AY166680.1	Homo sapiens BRD4-NUT fusion onc...	46	0.90	
gi 24658603 gb BC038988.1	Homo sapiens, Similar to bromodo...	46	0.90	
gi 16589002 gb AF386649.1 AF386649	Homo sapiens bromodomain...	46	0.90	
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gi 1477649 gb U63610.1 HSPLECTIN	Human plectin (PLEC1) gene...	46	0.90	
gi 3184497 gb AC004798.1 AC004798	Homo sapiens chromosome 1...	46	0.90	
gi 14704448 gb BC000156.1 BC000156	Homo sapiens, Similar to...	46	0.90	
gi 1296661 emb Z54367.1 HSPLECTIN	H.sapiens gene for plectin	46	0.90	
gi 16444668 emb AL139811.30	Human DNA sequence from clone ...	46	0.90	
gi 3115203 emb Y12059.1 HSHUNKI	H.sapiens HUNKI mRNA	46	0.90	

gi 392908 gb U00906.1 HSU00906	Human beta-spectrin (HSPTB1)...	46	0.90
gi 34495165 gb AC127350.3	Mus musculus chromosome 18 clone...	44	3.6
gi 29293996 gb AC080129.26	Homo sapiens 3 BAC RP11-135A1 (...)	44	3.6
gi 19747119 gb AC008533.9	Homo sapiens chromosome 5 clone ...	44	3.6
gi 26284723 gb AF550402.1 AF550396S7	Homo sapiens cob(I)ala...	44	3.6
gi 15145575 gb AC053503.7	Homo sapiens BAC clone RP11-316O...	44	3.6

Alignments

 Get selected sequences Select all Deselect all

>gi|9507134|ref|NM_019167.1|  Rattus norvegicus beta-spectrin 3 (Spnb3), mR
Length = 8178

Score = 383 bits (193), Expect = e-102

Identities = 193/193, (100%)

Strand = Plus / Plus

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Query: 253 ctgcgggacgggcgcaacctcctgaggctcgtggaggtgctctcgagagaccctgcca 312

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Identities = 191/193 (98%)

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Sbjct: 2011 gctctacttcatg 2023

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Strand = Plus / Plus

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Sbjct: 4646 aacattctgctaaagaagcaacagatgctggAACGAGAGATGGCTGTGAGAGAGAAGGGAG 4705

Query: 4293 gtagaggctatccaggcccaggccaaaagccctggcccaggaaagaccaaagtgcaggagag 4352
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 4706 gtagaggctatccaggcccaggccaaaagccctggcccaggaaagaccaaagtgcaggagag 4765

Score = 285 bits (144), Expect = 6e-73
Identities = 144/144 (100%)
Strand = Plus / Plus

Query: 1903 cgtcgtctctggagggttcctctgggaagtgggtgaggccgaggcctgggtcgggagcag 1962
|||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2312 cgtcgtctctggagggttcctctgggaagtgggtgaggccgaggcctgggtcgggagcag 2371

Query: 1963 cagcacccctggcctcagctgagacaggccggacactgactggtgtcctccgcctgctc 2022
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2372 cagcacccctggcctcagctgagacaggccggacactgactggtgtcctccgcctgctc 2431

Query: 2023 aataagcacacagccctacggggt 2046
||||||||||||||||||||||||
Sbjct: 2432 aataagcacacagccctacggggt 2455

Score = 278 bits (140), Expect = 1e-70
Identities = 143/144 (99%)
Strand = Plus / Plus

Query: 2719 gacatagctgagcagttgctgaaggccagtccaccaggcaaggaccgcattggcacc 2778
||||||||||||||||||||||||||||||||||||||||
Sbjct: 3128 gacatagctgagcagttgctgaaggccagtccaccaggcaaggaccgcattggcacc 3187

Query: 2779 caggagcagctaaccaaagggtggcagcagttcaggtccctggcaggtggcaaaaaggca 2838
||||||||||||||||||||||||||||||||||||||||
Sbjct: 3188 caggagcagctaaccaaagggtggcagcagttcaggtccctggcagatggcaaaaaggca 3247

Query: 2839 gctctgacatcagccctgagcatc 2862
||||||||||||||||||||
Sbjct: 3248 gctctgacatcagccctgagcatc 3271

Score = 246 bits (124), Expect = 5e-61
Identities = 141/147 (95%), Gaps = 6/147 (4%)
Strand = Plus / Plus

Query: 5285 gagtggaaaggacagtctaatgaggcctggctgacactgctggaggtggccctgctggac 5344
||||||||||||||||||||||||||||||||||||
Sbjct: 5711 gagtggaaaggacagtctaatgaggcctggctgacactgctggag-----ctgctggac 5764

Query: 5345 acaagaggtcaggtgctggctgtgttatgagctgcagcgcttcctgcatggggccgc 5404
||||||||||||||||||||||||||||
Sbjct: 5765 acaagaggtcaggtgctggctgtgttatgagctgcagcgcttcctgcatggggccgc 5824

Query: 5405 caagccctggcacgggtgcagcacaag 5431
||||||||||||||||||||
Sbjct: 5825 caagccctggcacgggtgcagcacaag 5851

Score = 240 bits (121), Expect = 3e-59
Identities = 121/121 (100%)
Strand = Plus / Plus

Query: 7091 gaaagagagcgagaaaaacgattcagctttaagaagaacaagtagttggggcaagac 7150
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7511 gaaagagagcgagaaaaacgattcagctttaagaagaacaagtagttggggcaagac 7570

Query: 7151 tcccaggccagctccctccctgttcagggaaactgccaggactgtcgacagagaccac 7210
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 7571 tcccaggccagctccctccctgttcagggaaactgccaggactgtcgacagagaccac 7630

Query: 7211 c 7211
|
Sbjct: 7631 c 7631

Score = 222 bits (112), Expect = 7e-54
Identities = 135/144 (93%), Gaps = 9/144 (6%)
Strand = Plus / Plus

Query: 673 tttgagtccctgaagaagtgtAACGcacactacaatctgcagaatgcttcaatctggct 732
||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1064 tttgagtccctgaagaagtgtAACGcacactacaatctgcagaatgcttcaatctggct 1123

Query: 733 gaaaaggaacttggcctgacgaagctcctggatcct-----aacgttagaccaaccc 783
||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1124 gaaaaggaacttggcctgacgaagctcctggatcctgaagatgtgaacgttagaccaaccc 1183

Query: 784 gatgagaagtccatcatcacctac 807
||||||||||||||||||||
Sbjct: 1184 gatgagaagtccatcatcacctac 1207

Score = 204 bits (103), Expect = 2e-48
Identities = 126/135 (93%), Gaps = 9/135 (6%)
Strand = Plus / Plus

Query: 6551 atgccccagagcagatcgtctgagtcagctcatgttgcacccctgcccgcacgagggtct 6610
||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 6971 atgccccagagcagatcgtctgagtcagctcatgttgcacccctgcccgcacgagggtct 7030

Query: 6611 gagctctctgctcaggaacagatgaaagg-----cgccaaacaggagatgaaagcc 6661
||||||||||||||||||||||||||||
Sbjct: 7091 gagctctctgctcaggaacagatgaaaggacgtgtgcgccaaacaggagatgaaagcc 7090

Query: 6662 ttcaataagaaagct 6676
||||||||||||||||
Sbjct: 7091 ttcaataagaaagct 7105

Score = 180 bits (91), Expect = 2e-41
Identities = 91/91 (100%)



results of BLAST

BLASTX 2.2.6 [Apr-09-2003]

genom.2

RID: 1069188234-32305-140862554207.BLASTQ3

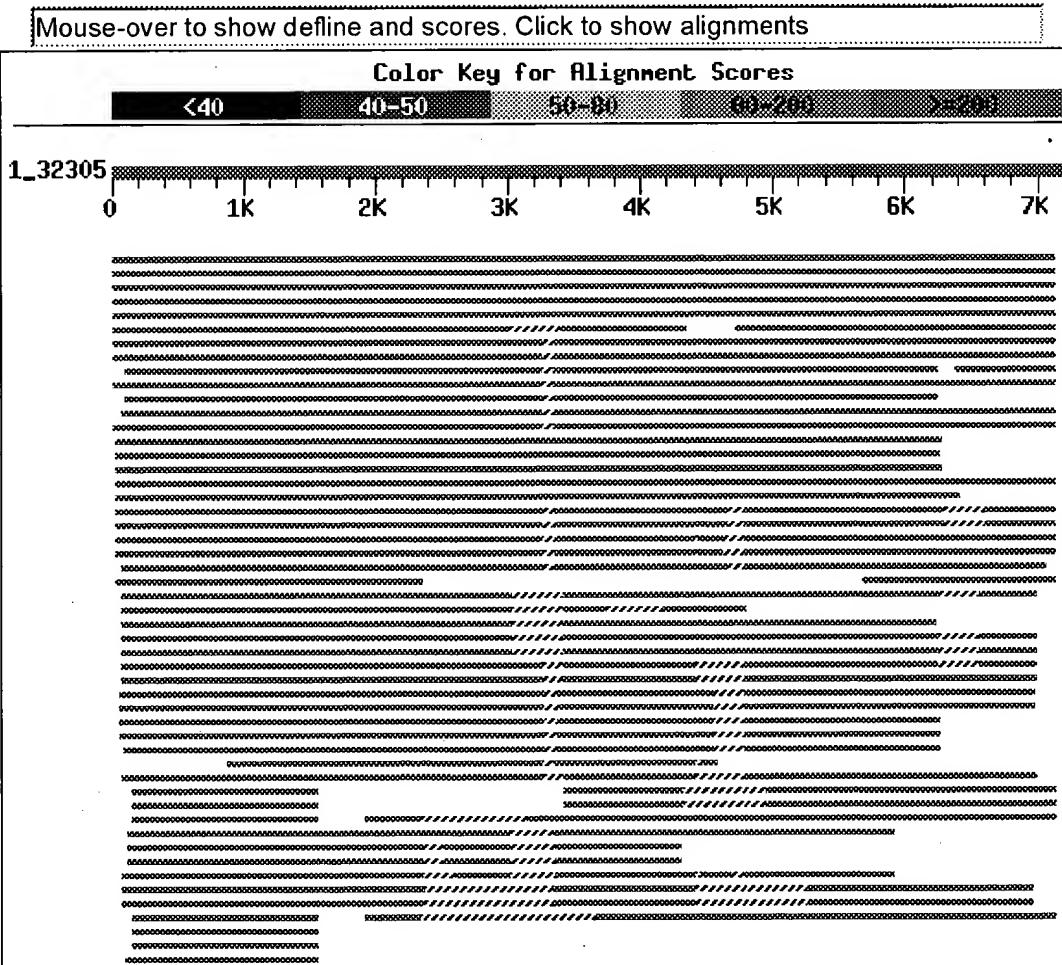
Query=

(7211 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,541,362 sequences; 503,870,249 total letters

Taxonomy reports

Distribution of 389 Blast Hits on the Query Sequence



Sequences producing significant alignments:

gi 11066461 qb AAG28596.1	spectrin-like protein GTRAP41 [R...	1071	0.0	
gi 17367415 sp Q9QWN8 SPCP RAT	Spectrin beta chain, brain 2...	1059	0.0	
gi 38084794 ref XP_129130.3	spectrin beta 3 [Mus musculus]	1058	0.0	
gi 9507135 ref NP_062040.1	beta-spectrin 3 [Rattus norvegi...	1057	0.0	
gi 5902122 ref NP_008877.1	spectrin, beta, non-erythrocyti...	1018	0.0	
gi 30348966 ref NP_787030.1	spectrin beta 2 isoform 1; bet...	711	0.0	
gi 4507195 ref NP_003119.1	spectrin, beta, non-erythrocyti...	709	0.0	
gi 30315658 ref NP_842565.1	spectrin, beta, non-erythrocyt...	699	0.0	
gi 448251 prf 1916380A	beta spectrin (beta fodrin)	698	0.0	
gi 7106421 ref NP_033286.1	spectrin beta 2 isoform 2; beta...	696	0.0	
gi 34879632 ref XP_240072.2	similar to Spectrin beta chain...	696	0.0	
gi 18859423 ref NP_571600.1	spectrin, beta, erythrocytic; ...	577	0.0	
gi 34866100 ref XP_234322.2	similar to Spectrin beta chain...	553	0.0	
gi 27413156 ref NP_000338.2	spectrin, beta, erythrocytic (...)	561	0.0	
gi 134798 sp P11277 SPCB HUMAN	Spectrin beta chain, erythro...	560	0.0	
gi 338440 qb AAA60578.1	spectrin Rouen (beta-220-218) muta...	561	0.0	
gi 7363453 ref NP_038703.1	spectrin beta 1; beta-spectrin ...	548	0.0	
gi 17647191 ref NP_523388.1	beta Spectrin CG5870-PA [Droso...	520	0.0	
gi 423777 pir A46147	spectrin beta chain - fruit fly (Dros...	520	0.0	
gi 29179635 qb AAH48851.1	Similar to beta-spectrin 3 [Mus ...	721	0.0	
gi 28277312 qb AAH46267.1	Similar to spectrin, beta, non-e...	741	0.0	
gi 476928 pir A47213	beta-fodrin - human (fragment) >gi 42...	423	0.0	
gi 15213122 qb AAK85734.1	beta-G spectrin [Brugia malayi]	470	e-177	
gi 17976528 qb AAK77612.2	Uncoordinated protein 70, isofor...	444	e-161	
gi 5734146 gb AAD49858.1	beta-G spectrin [Caenorhabditis e...	444	e-161	
gi 17562506 ref NP_504748.1	beta-G spectrin, UNCoordinated...	444	e-161	
gi 25154697 ref NP_504749.2	beta-G spectrin, UNCoordinated...	444	e-161	
gi 7505762 pir T29140	hypothetical protein K11C4.3 - Caeno...	442	e-161	
gi 31201697 ref XP_309796.1	ENSANGP00000012507 [Anopheles ...	517	e-144	
gi 31201699 ref XP_309797.1	ENSANGP00000023406 [Anopheles ...	517	e-144	
gi 226515 prf 1516310A	beta spectrin	461	e-128	
gi 13435161 ref NP_079489.1	spectrin, beta, non-erythrocyt...	461	e-127	
gi 11602887 qb AAF93171.1	betaIV spectrin isoform sigma2 [...]	461	e-127	
gi 11602890 qb AAF93173.1	betaIV spectrin isoform sigma4 [...]	459	e-127	
gi 11992162 qb AAG42473.1	spectrin beta IV [Homo sapiens]	458	e-127	
gi 17368942 sp Q9H254 SPCO HUMAN	Spectrin beta chain, brain...	458	e-127	
gi 30794220 ref NP_115999.1	spectrin beta 4; beta-spectrin...	458	e-127	
gi 16117405 qb AAK38731.1	beta4-spectrin [Mus musculus] >g...	458	e-127	
gi 338330 qb AAA63259.1	muscle beta spectrin	259	e-123	
gi 34855389 ref XP_218364.2	similar to betaIV-spectrin sig...	411	e-112	
gi 2511779 qb AAC79502.1	beta III spectrin [Homo sapiens]	390	e-106	
gi 444793 prf 1908227A	beta spectrin	320	2e-85	
gi 420115 pir S29854	spectrin beta chain - dog (fragment) ...	316	5e-84	
gi 18481635 qb AAL73492.1	beta I spectrin form betaI sigma...	245	5e-75	
gi 24656802 ref NP_523900.1	Karst CG12008-PA [Drosophila m...	258	9e-67	
gi 7655 emb CAA37939.1	betaH spectrin [Drosophila melanoga...	258	9e-67	
gi 103502 pir A37792	spectrin beta-H chain - fruit fly (Dr...	258	1e-66	
gi 31209523 ref XP_313728.1	ENSANGP00000017034 [Anopheles ...	250	2e-64	

gi 25155104 ref NP_741632.1	small body size SMA-1, betaH c...	246	6e-63	█
gi 7506776 pir T23630	hypothetical protein R31.1 - Caenorh...	246	6e-63	█
gi 13123941 sp Q9QXQ0 AAC4_RAT	Alpha-actinin 4 (Non-muscle ...	213	4e-53	█
gi 11230802 ref NP_068695.1	actinin alpha 4 [Mus musculus]...	213	5e-53	█
gi 38197444 gb AAH61788.1	Actn4 protein [Rattus norvegicus]	213	5e-53	█
gi 12025678 ref NP_004915.2	actinin, alpha 4 [Homo sapiens...	212	7e-53	█
gi 2804273 dbj BAA24447.1	alpha actinin 4 [Homo sapiens]	212	7e-53	█
gi 2493432 sp Q9C734 AAC4_CHICK	Alpha-actinin 4 (Non-muscle...	211	2e-52	
gi 32766291 gb AAH54901.1	Unknown (protein for MGC:63508) ...	207	2e-51	
gi 24639238 ref NP_477484.2	alpha actinin CG4376-PA [Droso...	204	2e-50	█
gi 13928936 ref NP_113863.1	alpha actinin 4; alpha actinin...	204	2e-50	█
gi 17565034 ref NP_506128.1	actinin (104.1 kD) (atn-1) [Ca...	203	3e-50	█
gi 24639240 ref NP_726784.1	alpha actinin CG4376-PB [Droso...	202	7e-50	█
gi 13124689 sp P18091 AACT_DROME	Alpha-actinin, sarcomeric ...	202	1e-49	█
gi 1070611 pir FAFFAA	alpha-actinin - fruit fly (Drosophil...	201	1e-49	
gi 31242387 ref XP_321624.1	ENSANGP00000011796 [Anopheles ...	201	2e-49	
gi 2511781 gb AAC79503.1	beta III spectrin [Homo sapiens]	201	2e-49	
gi 8186 emb CAA36042.1	unnamed protein product [Drosophila...	200	3e-49	█
gi 3157976 gb AAC17470.1	alpha actinin [Homo sapiens]	199	5e-49	█
gi 17137758 ref NP_477485.1	alpha actinin CG4376-PC [Droso...	198	1e-48	█
gi 25992501 gb AAN77132.1	alpha-actinin [Danio rerio] >gi ...	198	1e-48	
gi 211077 gb AAA48567.1	actinin [Gallus gallus]	196	7e-48	█
gi 13124665 sp P05094 AAC1_CHICK	Alpha-actinin 1 (Alpha-act...	196	7e-48	
gi 539494 pir A42162	alpha-actinin 1 - chicken >gi 211083 ...	196	7e-48	█
gi 32766313 gb AAH54911.1	Unknown (protein for MGC:63559) ...	196	7e-48	
gi 37362178 gb AAQ91217.1	actinin, alpha 2 [Danio rerio]	195	9e-48	
gi 38018016 gb AAR08137.1	brain-specific alpha actinin 1 i...	193	3e-47	█
gi 13591902 ref NP_112267.1	actinin, alpha 1; non-muscle a...	193	3e-47	█
gi 30585329 gb AAP36937.1	Homo sapiens actinin, alpha 1 [s...	192	1e-46	
gi 4501891 ref NP_001093.1	actinin, alpha 1 [Homo sapiens]...	192	1e-46	█
gi 32766260 gb AAH54830.1	Unknown (protein for MGC:62771) ...	192	1e-46	
gi 112959 sp P12814 AAC1_HUMAN	Alpha-actinin 1 (Alpha-actin...	192	1e-46	█
gi 63389 emb CAA32079.1	fibroblast alpha actinin [Gallus g...	192	1e-46	█
gi 23394914 gb AAN31639.1	alpha-actinin [Biomphalaria glab...	191	2e-46	
gi 28193204 emb CAD62344.1	unnamed protein product [Homo s...	191	2e-46	
gi 34876265 ref XP_214499.2	similar to actinin, alpha 2 [R...	189	5e-46	█
gi 4501893 ref NP_001094.1	actinin, alpha 2 [Homo sapiens]...	189	5e-46	█
gi 31981445 ref NP_150371.2	actinin alpha 2 [Mus musculus]...	189	6e-46	█
gi 32449722 gb AAH43995.2	Similar to actinin, alpha 1 [Xen...	188	1e-45	
gi 4557241 ref NP_001095.1	skeletal muscle specific actini...	187	2e-45	█
gi 112955 sp P20111 AAC2_CHICK	Alpha-actinin 2 (Alpha actin...	187	2e-45	
gi 19173800 ref NP_596915.1	actinin alpha 3 [Rattus norveg...	185	9e-45	█
gi 7304855 ref NP_038484.1	actinin alpha 3 [Mus musculus] ...	185	9e-45	█
gi 20853961 gb AAM26632.1	truncated alpha-actinin [Rattus ...	185	9e-45	█
gi 13123947 sp Q9J191 AAC2_MOUSE	Alpha-actinin 2 (Alpha act...	184	2e-44	█
gi 555419 gb AAA48566.1	alpha-actinin	184	3e-44	█
gi 7706190 ref NP_057726.1	spectrin, beta, non-erythrocyti...	182	8e-44	█
gi 31242389 ref XP_321625.1	ENSANGP00000023605 [Anopheles ...	182	1e-43	
gi 2137272 pir I49290	dystonin - mouse (fragment) >gi 9040...	174	3e-41	█

gi 19882219 ref NP_598594.1 	dystonin isoform a; bullous pe...	<u>174</u>	3e-41	
gi 19882221 ref NP_604443.1 	dystonin isoform b; bullous pe...	<u>174</u>	3e-41	
gi 30315911 sp Q60824_1	[Segment 1 of 2] Bullous pemphigoi...	<u>173</u>	4e-41	

Alignments

[Get selected sequences](#) [Select all](#) [Deselect all](#)

>[gi|11066461|gb|AAG28596.1|](#) spectrin-like protein GTRAP41 [Rattus norvegicus]
Length = 2388

Score = 1071 bits (2770), Expect(3) = 0.0
Identities = 750/1295 (57%), Positives = 760/1295 (58%), Gaps = 210/1295 (16%)
Frame = +1

Query: 1	MSSTLSPTDFDSLEIQ-----WDLPDSD-----LFERSRIRQYSDINNRSSS	126			
	MSSTLSPTDFDSLEIQ	WDLPDSD	LFERSRI+	+D	
Sbjct: 1	MSSTLSPTDFDSLEIQGQYSDINNRWDLPDSDWDNDSSARLFERSRIKALAD-----	53			
Query: 127	ARDEREAVQKKTFTWDNDKALAKWVNSHLARVTCRVDLYSXXXXXXXXXEVLSGET	306			
	EREAVQKKTFT	KWVNNSHLARVTCRVDLYS	EVLSGET		
Sbjct: 54	---EREAVQKKTFT-----KWVNNSHLARVTCRVDLYSDLRDGRNLLRLLEVLSGET	102			
Query: 307	LPKPTKGRMRIHCLENVDKALQFLKE---LENMGSHDIVDGQKVHNHRLTLGLVWTIIL	474			
	LPKPTKGRMRIHCLENVDKALQFLKE	LENMGSHDIVDG	NHRLTLGLVWTIIL		
Sbjct: 103	LPKPTKGRMRIHCLENVDKALQFLKEQKVHLENMGSHDIVDG---NHRLTLGLVWTIIL	158			
Query: 475	RF-----EDNKEKK-----CQMKTAGQIQDISVETDALLWVNHNFSAKY-	597			
	RF	EDNKEKK	CQMKTAG	VNVHNF+	+
Sbjct: 159	RFQIQDISVETEDNKEKKSADALLWQCQMKTAGYPN-----VNVHNFTTSWR	206			
Query: 598	PNLAFNAIVHKHRPDLLDTTSWRDGFEISLKKCNAHYNLQNAFNLAEKELGLTKLLDP---	768			
	LAFNAIVHKHRPDLLD	FESLKKCNAHYNLQNAFNLAEKELGLTKLLDP			
Sbjct: 207	DGLAFNAIVHKHRPDLLD-----FESLKKCNAHYNLQNAFNLAEKELGLTKLLDPEDV	259			
Query: 769	NVDQPDEKSIITYKMKALAVEDVVSTYYHYFS-----RIGKVLDHAMEAEASELL	918			
	NVDQPDEKSIITY	V+TYYHYFS	RIGKVLDHAMEAE		
Sbjct: 260	NVDQPDEKSIITY-----VATYYHYFSKMKALAVEGKRIGKVLDHAMEAE-----	304			
Query: 919	QWEGKHLVEKYESL-----TIGTFNDRQLANS---VQNQLQSFNSYRTIEQLSGV	1059			
	HLVEKYESL	TIGTFNDRQLANS	VQNQLQSFNSYRT	V	
Sbjct: 305	-----HLVEKYESLASELLQWIEQTIGTFNDRQLANSLSGVQNQLQSFNSYRT-----V	353			
Query: 1060	EKPPKFTEKGNLEVL---IQSKL RANNQKVY---EGRLILFTTPRS DINKAWERLEKAH	1221			
	EKPPKFTEKGNLEVL	IQSKL RANNQKVY	EGRLI	SDINKAWERLEKAH	
Sbjct: 354	EKPPKFTEKGNLEVLFTIQSKL RANNQKVYTPREGRLI-----SDINKAWERLEKAH	407			
Query: 1222	ERELALRTEAARFDRENQRLVIRQEKEQL-----RETWLS-----FGL	1341			
	ERELALRTE	LIRQEKEQL	RETWLS	FGL	
Sbjct: 408	ERELALRTE-----LIRQEKEQLAARFDRKAAMRETWLSENQRLVSDNFGL	455			
Query: 1342	ELAKAAAMSQDNRKHEAIETDIVAYSGRXXXXXXXXXXXXXXHYHDIKRIAARQN	1521			
	EL AA+	RKHEAIETDIVAYSGR	HYHDIKRIAARQN		
Sbjct: 456	EL--AAVEAAVRKHEAIETDIVAYSGR-----VQAVDAVAAELAAEHYHDIKRIAARQN	507			

Query: 1522 NVARLWDFLREMVAAXXXXXXXXXXXXXQKVFDQLLYLMQSQDLGQLHELVDWMAEMKGRL- 1698
 NVARLWDFLREMVAQKVFDQLLYLM DWMAEMKGRL
 Sbjct: 508 NVARLWDFLREMVAARRERLLNLELQKVFDQLLYLM-----DWMAEMKGRLQ 555

Query: 1699 -----KHLAGVEDLLEY-----IAVQAERVRAVSAYRPCGEQSYESALRFCDPGKEXX 1842
 KHLAGVEDLL+ IAVQAERVRAVSA SALRFCDPGKE
 Sbjct: 556 SQDLGKHLAGVEDLQLHELVEADIAVQAERVRAVSA-----SALRFCDPGKEYR 605

Query: 1843 -----XXXXXXXXXPQLVSALCEL-----RRLWRFLWEVGEAEAWVREQQHLLA 1977
 Q ALCEL RRLWRFLWEVGEAEAWVREQQHLLA
 Sbjct: 606 PCGPQLVSVRATLEQSYEALCELAATRRARLEESRRLWRFLWEVGEAEAWVREQQHLLA 665

Query: 1978 SAETGRDLTGVLRLNKHTALRGLTLEQGNQASTEMSGRLGPLK-----QQLVAEGHPG 2139
 SAETGRDLTGVLRLNKHTALRG EMSGRLGPLK QQLVAEGHPG
 Sbjct: 666 SAETGRDLTGVLRLNKHTALRG-----EMSGRLGPLKLTLEQGQQLVAEGHPG 714

Query: 2140 ALQXXXXXXXXX-----XXXXXXXXXXXXXSLYQFLVDALRQADANDMEAW----- 2286
 A Q SLYQF QADANDMEAW
 Sbjct: 715 ANQASTRAAELOAQWERLEALAEERAQRLAQASLYQF-----QADANDMEAWLVDALR 768

Query: 2287 LVSSPEVGHDEFSTQA-----RALEEEIXXXXXXXXXXQHPTLDALREQAA----- 2430
 LVSSPEVGHDEFSTQA RALEEEI PTLDALREQAA
 Sbjct: 769 LVSSPEVGHDEFSTQALARQHRALEEEI-----RAHRPTLDALREQAAALPPALS 818

Query: 2431 ---EVQGRVPTLEQRARALLSHTPHYEEILQARAGE-----FYTMLSEPGACNXXX 2571
 EVQGRVPTLEQ HYEELQARAGE FYTMLSE GAC
 Sbjct: 819 HTPEVQGRVPTLEQ-----HYEELQARAGERARALEAALAFYTMLSEAGACG--- 865

Query: 2572 XXXXXXXXWVEEKEQWL-----DPEVVQQRFETITAVSPERLELEPEMNALAAR- 2718
 WVEEKEQWL DPEVVQQRFET LEPEMNALAAR
 Sbjct: 866 -----LWVEEKEQWLNGLALPERLEDPEVVQQRFET-----LEPEMNALAARI 908

Query: 2719 ----DIAEQLLKASPPGKDRIIGTQEQLNQRWQQFRSLAGGKKAALTSALSI----- 2862
 DIAEQLLKASPPGKDRIIGTQEQLNQRWQQFRSLAGGKKAALTSALSI
 Sbjct: 909 TAVSDIAEQLLKASPPGKDRIIGTQEQLNQRWQQFRSLAGGKKAALTSALSIQNYHLECT 968

Query: 2863 ETQAWMRE-----QDLGNLQAQNYHLECTKTVIESTGVIALQRKLAGTERDL*ADP 3018
 ETQAWMRE QDLGNLA GVLALQRKLAGTERDL A
 Sbjct: 969 ETQAWMRETKVIESTQDLGNLA-----GVLALQRKLAGTERDLEA-I 1011

Query: 3019 RAK*SHLCPGFGCWAPS PSCPQHTMGGSSGNPGLARRLGEVQ-----TMRRREES 3174
 A+ L A P+ P + RLGEVQ TMRRREES
 Sbjct: 1012 SARVGEILTQEANALAAGHPAQA-----PAINTRLGEVQTGWEDLRATMRRREES 1060

Query: 3175 -----DFLRSLDDFQAWLGRLQTQAVASYE 3255
 DFLRSLDDFQAWLGR TQAVAS E
 Sbjct: 1061 LGEARRLQDFLRSLDDFQAWLGR---TQAVASEE 1092

Score = 740 bits (1910), Expect(3) = 0.0
 Identities = 536/931 (57%), Positives = 545/931 (58%), Gaps = 144/931 (15%)
 Frame = +2

Query: 4775 QAWMGEQE-----KAKDELSAQ-----VLEQALALHMMGQEQAEVKKHDYAQTIQ 4912
 +AWMGEQE KAKDELSAQ VLEQALA DYAQTIQ
 Sbjct: 1601 EAWMGEQELHMMGQEKAQDELSAQAEVKKHQVLEQALA-----DYAQTIQ 1646

Query: 4913 LAASSQDMIDHEHPESTRLTIRGLKELAQAVDKLYA-----RERLQEHLRLCQXX 5065
 LAASSQDMIDHEHPESTRLTIR QAQVDKLYA RERLQEHLRLCQ

Sbjct: 1647 LAASSQDMIDHEHPESTRLTIR-----QAQVDKLYAGLKELAGERRERLQEHLRLCQLR 1700
 Query: 5066 XXXXXXXX-----XXXXXSHELGQDYEH-----HEQWIQERVTMLRDKFREFSRDTDSXXXXXXX 5230
 SHELGQDYEH VTMLRDKFREFSRDT
 Sbjct: 1701 RELDDLEQWIQEREREVVAASHELGQDYEH-----VTMLRDKFREFSRDT----- 1743
 Query: 5231 XTSTIGQERV-----NGLIAGGH-----EWKDSLNEAWADLLEVALLDTRGQVLAA 5368
 STIGQERV NGLIAGGH EWKDSLNEAWADLLE LLDTRGQVLAA
 Sbjct: 1744 --STIGQERVDSANALANGLIAGGHAATVAEWKDSLNEAWADLLE--LLDTRGQVLAA 1799
 Query: 5369 AYELQRFLH GARQALARVQHKA AEALQRQQLPDGTGRDLNEHDD-DGRHCAYVQQVQIQ 5545
 AYELQRFLH GARQALARVQHK QQQLPDGTGRDLN + RHCAY + IQ
 Sbjct: 1800 AYELQRFLH GARQALARVQHK-----QQQLPDGTGRDLNAAEALQRRHCAY--EHDIQ 1850
 Query: 5546 ALSTQ-----LRLQKAYAGDKA QEIQLQTTDGRHMQXXX---XXXXXXXXXRRQLLL 5692
 ALSTQ LRLQKAYAGDKA+EI GRHMQ RRQLLL
 Sbjct: 1851 ALSTQVQQVQDDGLRLQKAYAGDKAEEI-----GRHMQAVAEAWAQLQGSSAARRQLLL 1904
 Query: 5693 ---DKFREFFKAVREMLWMAQERPRDKNQQGIKDGINLQM-----DVSSADLVI--- 5830
 DKFREFFKAVREMLWM DGINLQM DVSSADLVI
 Sbjct: 1905 DTTDKFREFFKAVREMLWM-----DGINLQMADAQERPRDVSSADLVIKNQQ 1950
 Query: 5831 ---AEIEARADRFSACID-----RNHYAAEELQSRRMGQELLAISEKLSQ----- 5956
 AEIEARADRFSACID RNHYAAEE ISEKLSQ
 Sbjct: 1951 GIKAEIEARADRFSACIDMGQELLARNHYAAEE-----ISEKLSQLQSRRQET 1998
 Query: 5957 AEKWQEKM DWXXXXXXXXXXXXXFGRDAGMAEAWLGCEAFLCSQEPLV RSA-----E 6109
 AEKWQEKM DW FGRDAGMAEAW LCSQEPLV RSA E
 Sbjct: 1999 AEKWQEKM DW---LQLVLEVLFGRDAGMAEAW-----LCSQEPLV RSAELGCTVDEVE 2049
 Query: 6110 SLIKRHTVDEVEQKSAVAWEERFSALEKL TALQERENEQKRKPTSEPRYEE*RRKQP--- 6280
 SLIKRH E QKSAVAWEERFSALEKL TAL+ERENEQKRK R EE RRKQP
 Sbjct: 2050 SLIKRH---EAFQKSAVAWEERFSALEKL TALEERENEQKRK-----REEEERRKQPPTS 2101
 Query: 6281 -----PEGSLVDGQRVXHPT-QSMASQLDTATQAPSINGVCTDKLPPSTESSQPLLEQQ 6439
 PEGSLVDGQRV S+L +TQAPSINGVCTD TESSQPLLEQQ
 Sbjct: 2102 EPMA S QPEGSLVDGQRV LDTAWDGTQSKLPPSTQAPSINGVCTD-----TESSQPLLEQQ 2156
 Query: 6440 RLEQSNVXXXXXXXXXXXXXXXXXXXXXDRVERQTLPR-----MPQSRSSSEAHVATLPA 6601
 RLEQSNV R ERQTLPR MPQSRSSSEAHVATLPA
 Sbjct: 2157 RLEQSNVP-----EGPGSGTGDESSGPRGERQTLPRGPAPSPMPQSRSSESAHVATLPA 2210
 Query: 6602 RGAELSAQE QMEG---RKQEMEAFNKKAYCVLRRGTL CANRSWQNV-----SLGFYKD 6751
 RGAELSAQE QMEG RKQEMEAFNKA ANRSWQNV SLGFYKD
 Sbjct: 2211 RGAELSAQE QMEG TL CRK QEMEAFNKA-----ANRSWQNVYCVLRRGSLGFYKD 2260
 Query: 6752 ARAASAGV SLARAQGKRKH VFKLPYHGEVPV-----SVAFDYR-----GLQDGKE 6886
 ARAASAGV PYHGEVPV SVAFDYR GLQDGKE
 Sbjct: 2261 ARAASAGV-----PYHGEVPV SLARAQGS VAFD YRKRKH VFKL GLQDGKE 2305
 Query: 6887 YLFQARVVNAAIAKDEAEMSSWL-----TASSASGXXXXXXXXX DGRTRAMTMIV 7042
 YLFQ AKDEAEMSSWL TASSASG G TRAMTM
 Sbjct: 2306 YLFQ-----AKDEAEMSSWL RVVNAAIATASSASGEPEEPVVP SASRGLTRAMTMPP 2357
 Query: 7043 LRSKSASRGLS QPEGSEREREKRF SFFKKNK 7135
 + S L +G EREREKRF SFFKKNK
 Sbjct: 2358 VSQPEG SIVLRSKDG REREREKRF SFFKKNK 2388

Score = 496 bits (1278), Expect(3) = 0.0
 Identities = 347/585 (59%), Positives = 356/585 (60%), Gaps = 74/585 (12%)
 Frame = +3

Query: 3258 PSTLPRGETL---GXXXXXXXXXXXXXYSRLR-----QADPQCVERAQSEEVTRDR 3401
 P+TLP E L YSRLR QADPQC+ R
 Sbjct: 1094 PATLPEAEALLAQHAALRGEVERAQSEYSRLRTLGEEVTRDQADPQCLFL-----R 1144

Query: 3402 QRLEALGTGWEELGLFLRMWESRQGRLAQAHGFQGFLRNDARQAEGLTEMPGTKLEDFMS 3581
 QRLEALGTGWEELG RMWESRQGRLAQAHGFQGFLRNDARQAEGL S
 Sbjct: 1145 QRLEALGTGWEELG---RMWESRQGRLAQAHGFQGFLRNDARQAEGL-----S 1189

Query: 3582 SQEYVLSH-----LQAADAAIK-----STMDANGERIRGLLEAGRQLVSKGNIHAEKI 3725
 SQEYVLSH LQAADAAIK STMDANGERIRGLLEAGRQLVSKGNIHAEKI
 Sbjct: 1190 SQEYVLSHTEMPGTIQAADAAIKKLEDFMSTMDANGERIRGLLEAGRQLVSKGNIHAEKI 1249

Query: 3726 QEKAQDIEKRHRKNQEAVQQLLGRRLDNR---FLQDCQELKLIWVSYDEEQQHIDEKMLT 3893
 QEKAQDIEKRHRKNQEAVQQLLGRRLDNR FLQDCQELKLIW IDEKMLT
 Sbjct: 1250 QEKAQDIEKRHRKNQEAVQQLLGRRLDNRQQHFLQDCQELKLIW-----IDEKMLT 1300

Query: 3894 AQD-----HTKWQKHQAQFMDKVDKARNLAEALAANKDWL-----LTLEKPELK 4019
 AQD HTKWQKHQAQFMDKVDKARNLAEALAANKDWL LTLEKPELK
 Sbjct: 1301 AQDVSYDEARNLHTKWQKHQAQFMDKVDKARNLAEALAANKDWL-----LTLEKPELK 1351

Query: 4020 VLRWDELEGREVSEKLEDLHR-----QAKARSLFDANALESWETTTRAELFAQSCS 4172
 VL VSEKLEDLHR QAKARSLFDAN RAELFAQSCS
 Sbjct: 1352 VL-----VSEKLEDLHRRWDELETTQAKARSLFDAN-----RAELFAQSCS 1393

Query: 4173 -----LESLQAQLHSDDYGKDLTSVNILLKKQQMLEREMAVR*KEVEAIQQAQAKALAQED 4337
 LESLQAQLHSDDYGKDLTSVNILLKKQQMLEREMAVR KEVEAIQQAQAKALAQED
 Sbjct: 1394 ALESWLESLQAQLHSDDYGKDLTSVNILLKKQQMLEREMAVREKEVEAIQQAQAKALAQED 1453

Query: 4338 QSAGE---SRAVEEKFRALLQ--ASR*KDLSA-HEXXXXXXXXXXXXXTVGAAPGDRA 4496
 QSAGE SRAVEEKFRAL Q R + L A E P +
 Sbjct: 1454 QSAGEVERTSRAVEEKFRALCQPMKDRCCRRLQASREQHQFHRDVEDEILWVTERLPMASS 1513

Query: 4497 ASHGQLSGAWQEEKPDSAPDCRPQRQPAHDPGP*AHSEN-----TEGDRQAELO 4655
 HG+ + Q + Q L + H+P - E G AELO
 Sbjct: 1514 LEHGKDLPSVQLLMK-----KNQTLQKEIQGHEPRIADLKERQRTLRTAAAGPELAELO 1567

Query: 4656 EMWKRLSHELEAAAGPELLRGKRLEEALRAQQFYRDAEEARLGWG 4790
 EMWKRLSHELE LRGKRLEEALRAQQFYRDAEAEAA G
 Sbjct: 1568 EMWKRLSHELE-----LRGKRLEEALRAQQFYRDAEAEAWMG 1605

Score = 80.5 bits (197), Expect = 4e-13
 Identities = 54/98 (55%), Positives = 56/98 (57%), Gaps = 26/98 (26%)
 Frame = +1

Query: 4411 CQPMKDRCCR-----FHRDVEDEILWEQHQVTERLPMASSLEHGK-----KK 4536
 CQPMKDRCCR FHRDVEDEILW VTERLPMASSLEHGK KK
 Sbjct: 1474 CQPMKDRCCRRLQASREQHQFHRDVEDEILW---VTERLPMASSLEHGKDLPSVQLLMKK 1529

Query: 4537 NQTL-----PRIADLKDLPSVQLLMIQGHERTLRT 4626
 NQTL PRIADLK+ +RTLRT
 Sbjct: 1530 NQTLQKEIQGHEPRIADLKE-----RQRTLRT 1556

Score = 37.4 bits (85), Expect = 4.1
 Identities = 41/168 (24%), Positives = 72/168 (42%), Gaps = 13/168 (7%)
 Frame = +2

Query: 5675 RRQLLLDKFRFFKAVRELMLWMAQERPRDKNQQGIKDGINLQMDVSSADLVIASIEARAD 5854
 R Q ++ +F + V + +LW+ + P + + KD ++Q+ + + EI+
 Sbjct: 1483 RLQASREQHQFHRDVEDEILWVTERLPMASSLEHGKDLPSVQLLMKKNQTLQKEIQGHEP 1542

Query: 5855 RFSACIDRNHYAAE-----ELQS--RRMGQELLAISEKLSQAEKWQEKMDWXXXXXX 6004
 R + +R ELQ +R+ EL ++L +A + Q+
 Sbjct: 1543 RIADLKERQRTLRTAAAGPELAELQEMWKRLSHELELRGKRLEALRAQQ----- 1592

Query: 6005 XXXXXXFGRDAGMAEAWLG-CEAFLCSQEPL--VRSAESLIKRHTVDE 6139
 F RDA AEAW+G E + QE SA++ +K+H V E
 Sbjct: 1593 -----FYRDAAEAEAWMGEQELHMMGQEAKDELSAQAEVKKHQVLE 1634

Score = 37.0 bits (84), Expect = 5.4
 Identities = 70/325 (21%), Positives = 125/325 (38%), Gaps = 15/325 (4%)
 Frame = +3

Query: 3405 RLEALGTGWEELGLFLRMWESRQGRLAQAHGFQGFLRNDARQAEGLTEMPGTKLEDFMSS 3584
 R L WE L E R RLAQA F DA E L + +
 Sbjct: 721 RAAELQQAWERLEALA--EERAQRLAQAAASLYQFQADANDMEAWLVDALRLVSSPEVGH 777

Query: 3585 QEYVLSHLQAADAAIKSTMMDANGERIRGLLEAGRQLVSKGNIHAEKIQEKADSIEKRHRK 3764
 E+ L A++ + A+ + L E L + H ++Q + ++E+ + +
 Sbjct: 778 DEFSTQALARQHRALEEEIRAHRPTLDALREQAAALPPALS-HTPEVQGRVPTLEQHYEE 836

Query: 3765 NQ----EAVQQLLGRRLRDNRFLQDCQELKLWVSYDEE-----QQHIDEKMLTAQDHT 3908
 Q E + L L L + LWV E+ ++ D +++ + T
 Sbjct: 837 LQARAGERARALEAALAFYTMSEAGACGLWVEEKEQWLNGLALPERLEDPEVVQQRFET 896

Query: 3909 KWQKHQAFMDKVDKARNLAE LAANKDWLLTLEKPELKVLRWDELEGREVSEKLEDLHRQA 4088
 + A ++ ++AE LL P + + + + ++ L
 Sbjct: 897 LEPEMNALAARITAVSDIAEQ----LLKASPPGKDRIIGTQEQLNQRWQQFRSLAGGK 950

Query: 4089 KARSILFDANALESWE---TTTRAELFAQSCSLESLQQLHSDDYGKDLTSVNILLKKQOM 4259
 KA +L A +++++ T T+A + ++ +ES Q D G DL V
 Sbjct: 951 KA-ALTSALSIQNYHLECTETQAWMREKTKVIESTQ----DLGNDLAGV----LA 996

Query: 4260 LEREMAVR*KEVEAIQQAQAKALAQE 4334
 L+R++A +++EAI A+ L QE
 Sbjct: 997 LQRKLAGTERDLEAISARVGELETQE 1021

Score = 36.6 bits (83), Expect = 7.0
 Identities = 39/141 (27%), Positives = 58/141 (41%), Gaps = 4/141 (2%)
 Frame = +1

Query: 1636 SQDLGQLHELVDWMAEMKGRILKLAGVEDLLEYIAVQA---ERVRAVSAYRPCGEQSYE 1803
 +QDLG + +A + + LAG E LE I+ + + A++A P +
 Sbjct: 984 TQDLG-----NDLAGVLALQRKLAGTERDLEAISARVGELETQEANALAAGHPAQAPAIN 1037

Query: 1804 SALRFCDPGKXXXXXXXXXXXXPQLVSALCELRRILWRFLWEVGEAEAWVREQQHLLASA 1983
 + L G E +L E RRL FL + + +AW+ Q +AS
 Sbjct: 1038 TRLGEVQTGWEDLRATMRRRE-----ESLGEARRILQDFLRSI/DDFQAWLGRQTAVASE 1091

Query: 1984 ETGRDLTGVLRLLNKHTALRG 2046
 E L LL +H ALRG
 Sbjct: 1092 EGPATLPEAEALLAQHAALRG 1112

[]>gi|17367415|sp|Q9QWN8|SPCP RAT Spectrin beta chain, brain 2 (Spectrin, non-eryt
 (Beta-III spectrin) (SPNB-3) (Beta SpIII sigma 1)
 (Spectrin-like protein GTRAP41)
 gi|3550975|dbj|BAA32699.1| [] beta-spectrin III [Rattus norvegicus]
 Length = 2388

Score = 1059 bits (2738), Expect (3) = 0.0
 Identities = 746/1295 (57%), Positives = 756/1295 (58%), Gaps = 210/1295 (16%)
 Frame = +1

Query: 1 MSSTLSPTDFDSLEIQ-----WDLPDSD-----LFERSRIRQYS DINNRSSS 126
 MSSTLSPTDFDSLEIQ WDLPDSD LFERSRI+ +D
 Sbjct: 1 MSSTLSPTDFDSLEIQGQYS DINNRWDL PDSDWDNDSSSARLFERSRIKALAD----- 53

Query: 127 ARDEREAVQKKTFTWDNDKALAKWVN SHLARVTCRVDLYSXXXXXXXXXEVLSGET 306
 EREAVQKKTFT KWVN SHLARVTCRVDLYS EVLSGET
 Sbjct: 54 ---EREAVQKKTFT-----KWVN SHLARVTCRVDLYS DLRDGRNLLRLLEVLSGET 102

Query: 307 LPKPTKGRMRIHCLENVDKALQFLKE---LENMGSHDIVDGQKVHNHRLTLGLVWTIIL 474
 LPKPTKGRMRIHCLENVDKALQFLKE LENMGSHDIVDG NHRLTLGLVWTIIL
 Sbjct: 103 LPKPTKGRMRIHCLENVDKALQFLKEQKVHLENMGSHDIVDG---NHRLTLGLVWTIIL 158

Query: 475 RF-----EDNKEKK-----CQMKTAGQIQDISVETDALLWVN VHNFSAKY- 597
 RF EDNKEKK CQMKTAG VNVHNF+ +
 Sbjct: 159 RFQIQDISVETEDNKEKKSADALLWCQMKTAGY PN-----VNVHNFTTSWR 206

Query: 598 PNLAFAIVHKHRPDLLDTTSWRDG FESLKKCNAHYNLQNAFNLAEKELGLTKLLDP--- 768
 LAFNAIVHKHRPDLL FESLKKCNAHYNLQNAFNLAEKELGLTKLLDP
 Sbjct: 207 DGLAFNAIVHKHRPDLL-----FESLKKCNAHYNLQNAFNLAEKELGLTKLLDPEDV 259

Query: 769 NVDQPDEKSIITYKMKALAVEDVVSTYYHYFS-----RIGKVLDHAMEAEASELL 918
 NVDQPDEKSIITY V+TYYHYFS RIGKVLDHAMEAE
 Sbjct: 260 NVDQPDEKSIITY-----VATYYHYFS KMKALAVEGKRIGKVLDHAMEAE---- 304

Query: 919 QWEGKHLVEKYESL-----TIGTFNDRQLANS--VQNQLQSFNSYRTIEQLSGV 1059
 HLVEKYESL TI T NDRQLANS VQNQLQSFNSYRT V
 Sbjct: 305 -----HLVEKYESLASELLQWIEQTIVTLNDRQLANSLSGVQNQLQSFNSYRT-----V 353

Query: 1060 EKPPKFTEKGNLEVL---IQSKLRANNQKVY---EGRLILFTTPRS DINKAWERLEKAH 1221
 EKPPKFTEKGNLEVL IQSKLRANNQKVY EGRLI SDINKAWERLEKAH
 Sbjct: 354 EKPPKFTEKGNLEVLFTIQSKLRANNQKVYTPREGRLI-----SDINKAWERLEKAH 407

Query: 1222 ERELALRTEAARFDRENQRLVLIROEKLEQL-----RETWLS-----FGL 1341
 ERELALRTE LIRQEKLEQL RETWLS FGL
 Sbjct: 408 ERELALRTE-----LIRQEKLEQLAARFDRKAAMRETWLSENQRLVSDNFGL 455

Query: 1342 ELAKAAMSQDNRKHEAIETDIVAYSGRXXXXXXXXXXXXXXHYHDIKRIAARQN 1521
 EL AA+ RKHEAIETDIVAYSGR HYHDIKRIAARQN
 Sbjct: 456 EL--AAVEAAVRKHEAIETDIVAYSGR-----VQAVDAVAAELAEHYHDIKRIAARQN 507

Query: 1522 NVARLWDFLREMVAAXXXXXXXXXXQKV FQDLYLMQSQDLGQLHELV DWMAEMKGRL- 1698
 NVARLWDFLREMVAQKV FQDLYLM DWMAEMKGRL
 Sbjct: 508 NVARLWDFLREMVAARRERLLNLELQKV FQDLYLM-----DWMAEMKGRLQ 555

Query: 1699 -----KHLAGVEDLLEY-----IAVQAERVRAVSAYRPCGEQSYESALRFCDPGKEXX 1842
 KHLAGVEDLL+ IAVQAERVRAVSA SALRFCDPGKE
 Sbjct: 556 SQDLGKHLAGVEDLLQLHELVEADIAVQAERVRAVSA-----SALRFCDPGKEYR 605

Query: 1843 ----XXXXXXXXXPQLVSALCEL-----RRLWRFLWEVGEAEAWVREQQHLLA 1977
 Q ALCEL RRLWRFLWEVGEAEAWVREQQHLLA
 Sbjct: 606 PCDPQLVSVERVATLEQSYEALCELAATRRARLEESRRLWRFLWEVGEAEAWVREQQHLLA 665

Query: 1978 SAETGRDLTGVLRLNKHTALRGLTLEQGNQASTEMSGRLGPLK-----QQLVAEGHPG 2139
 SAETGRDLTGVLRLNKHTALRG EMSGRLGPLK QQLVAEGHPG
 Sbjct: 666 SAETGRDLTGVLRLNKHTALRG-----EMSGRLGPLKLTLEQGQQLVAEGHPG 714

Query: 2140 ALQXXXXXXXXX-----XXXXXXXXXXXXXXXXSLYQFLVDALRQADANDMEAW----- 2286
 A Q SLYQF QADANDMEAW
 Sbjct: 715 ANQASTRAAELQAQWERLEALAEERAQRLAQASLYQF-----QADANDMEAWLVDALR 768

Query: 2287 LVSSPEVGHDEFSTQA-----RALEEEIXXXXXXXXXXQHPTLDALREQAA----- 2430
 LVSSPEVGHDEFSTQA RALEEEI PTLDALREQAA
 Sbjct: 769 LVSSPEVGHDEFSTQALARQHRALEEEI-----RAHRPTLDALREQAAALPPALS 818

Query: 2431 ---EVQGRVPTLEQRARALLSHTPHYEELQARAGE-----FYTMLSEPGACNXXX 2571
 EVQGRVPTLEQ HYEELQARAGE FYTMLSE GAC
 Sbjct: 819 HTPEVQGRVPTLEQ-----HYEELQARAGERARALEAALAFYTMSEAGACG--- 865

Query: 2572 XXXXXXXXWVEEKEQWL-----DPEVVQQRFETITAVSPERLELEPEMNALAAR- 2718
 WVEEKEQWL D EVVQQRFET LEPEMNALAAR
 Sbjct: 866 -----LWVEEKEQWLNGLALPERLEDLEVVQQRFET-----LEPEMNALAARV 908

Query: 2719 ---DIAEQLLKASPPGKDRIIGTQEQLNQRWQQFRSLAGGKKAALTSALSI----- 2862
 DIAEQLLKASPPGKDRIIGTQEQLNQRWQQFRSLA GKKAALTSALSI
 Sbjct: 909 TAVSDIAEQLLKASPPGKDRIIGTQEQLNQRWQQFRSLADGKKAALTSALSIQNYHLECT 968

Query: 2863 ETQAWMRE-----QDLGNLDAQNYHLECTKTKVIESTGVIALQRKLAGTERDL*ADP 3018
 ETQAWMRE QDLGNLDA GVIALQRKLAGTERDL A
 Sbjct: 969 ETQAWMREKTKVIESTQDLGNLDA-----GVIALQRKLAGTERDLEA-I 1011

Query: 3019 RAK*SHLCPGGFGCWAPSPSPCHQHTMGGSSGNPLARRLGEVQ-----TMRRREES 3174
 A+ L A P+ P + RLGEVQ TMRRREES
 Sbjct: 1012 SARVGELETQEANALAAAGHPAQA-----PAINTRLGEVQTGWEDLRATMRRREES 1060

Query: 3175 -----DFLRSLDDFQAWLGRRLQTQAVASYE 3255
 DFLRSLDDFQAWLGR TQAVAS E
 Sbjct: 1061 LGEARRLQDFLRSLDDFQAWLGR---TQAVASEE 1092

Score = 740 bits (1910), Expect(3) = 0.0
 Identities = 536/931 (57%), Positives = 545/931 (58%), Gaps = 144/931 (15%)
 Frame = +2

Query: 4775 QAWMGEQE-----KAKDELSAQ-----VLEQALALHMMGQEQAEVKKHDYAQTIKQ 4912
 +AWMGEQE KAKDELSAQ VLEQALA DYAQTIKQ
 Sbjct: 1601 EAWMGEQELHMMGQEKAQDELSAQAEVKKHQVLEQALA-----DYAQTIKQ 1646

Query: 4913 LAASSQDMIDHEHPESTRLTIRGLKELAQQAQVDKLYA-----RERLQEHLRLCQXX 5065
 LAASSQDMIDHEHPESTRLTIR QAQVDKLYA RERLQEHLRLCQ
 Sbjct: 1647 LAASSQDMIDHEHPESTRLTIR-----QAQVDKLYAGLKELAGERRERLQEHLRLCQLR 1700

Query: 5066 XXXXXXXX-----XXXXXSHELGQDYEHQWIQERVTMLRDKFREFSRDTSXXXXXXX 5230



results of BLAST

```

# BLASTN 2.2.6 [Apr-09-2003]
# Query:
# Database: nr
# Fields: Query id, Subject id, % identity, alignment length, mismatches, gap openin
1_30527 gi|3452552|dbj|AB001347.1| 92.00 300 0 12 193 480
1_30527 gi|3452552|dbj|AB001347.1| 81.75 515 42 45 3633 4115
1_30527 gi|3452552|dbj|AB001347.1| 86.09 381 9 22 4173 4530
1_30527 gi|3452552|dbj|AB001347.1| 84.07 427 9 24 4142 4530
1_30527 gi|3452552|dbj|AB001347.1| 98.96 193 2 0 1440 1632
1_30527 gi|3452552|dbj|AB001347.1| 100.00 144 0 0 1903 2046
1_30527 gi|3452552|dbj|AB001347.1| 98.65 148 2 0 2719 2866
1_30527 gi|3452552|dbj|AB001347.1| 95.92 147 0 2 5285 5431
1_30527 gi|3452552|dbj|AB001347.1| 100.00 121 0 0 7091 7211
1_30527 gi|3452552|dbj|AB001347.1| 93.75 144 0 2 673 807
1_30527 gi|3452552|dbj|AB001347.1| 86.87 198 7 11 2686 2866
1_30527 gi|3452552|dbj|AB001347.1| 91.84 147 1 4 3398 3543
1_30527 gi|3452552|dbj|AB001347.1| 93.33 135 0 6 6551 6676
1_30527 gi|3452552|dbj|AB001347.1| 100.00 91 0 0 4888 4978
1_30527 gi|3452552|dbj|AB001347.1| 98.89 90 1 0 6146 6235
1_30527 gi|3452552|dbj|AB001347.1| 98.90 91 0 1 4709 4798
1_30527 gi|3452552|dbj|AB001347.1| 86.76 136 0 7 5624 5741
1_30527 gi|3452552|dbj|AB001347.1| 81.54 195 8 19 5561 5741
1_30527 gi|3452552|dbj|AB001347.1| 98.70 77 0 1 1176 1252
1_30527 gi|3452552|dbj|AB001347.1| 91.09 101 0 4 5957 6057
1_30527 gi|3452552|dbj|AB001347.1| 84.06 138 12 10 6865 6997
1_30527 gi|3452552|dbj|AB001347.1| 90.62 96 0 1 1057 1143
1_30527 gi|3452552|dbj|AB001347.1| 84.25 127 5 9 5024 5135
1_30527 gi|3452552|dbj|AB001347.1| 87.50 96 0 4 2143 2238
1_30527 gi|3452552|dbj|AB001347.1| 98.18 55 1 0 6406 6460
1_30527 gi|3452552|dbj|AB001347.1| 88.10 84 4 5 4610 4688
1_30527 gi|3452552|dbj|AB001347.1| 91.55 71 3 3 2937 3006
1_30527 gi|3452552|dbj|AB001347.1| 82.35 119 10 10 6281 6392
1_30527 gi|3452552|dbj|AB001347.1| 83.19 113 6 9 5453 5560
1_30527 gi|3452552|dbj|AB001347.1| 100.00 49 0 0 1375 1423
1_30527 gi|3452552|dbj|AB001347.1| 87.36 87 2 2 961 1038
1_30527 gi|3452552|dbj|AB001347.1| 100.00 48 0 0 604 651
1_30527 gi|3452552|dbj|AB001347.1| 100.00 48 0 0 1 48
1_30527 gi|3452552|dbj|AB001347.1| 100.00 47 0 0 3050 3096
1_30527 gi|3452552|dbj|AB001347.1| 100.00 45 0 0 6731 6775
1_30527 gi|3452552|dbj|AB001347.1| 100.00 45 0 0 5831 5875
1_30527 gi|3452552|dbj|AB001347.1| 100.00 45 0 0 5156 5200
1_30527 gi|3452552|dbj|AB001347.1| 84.38 96 0 8 2287 2367
1_30527 gi|3452552|dbj|AB001347.1| 100.00 42 0 0 1733 1774
1_30527 gi|3452552|dbj|AB001347.1| 100.00 39 0 0 865 903
1_30527 gi|3452552|dbj|AB001347.1| 100.00 36 0 0 6074 6109
1_30527 gi|3452552|dbj|AB001347.1| 100.00 36 0 0 3291 3326
1_30527 gi|3452552|dbj|AB001347.1| 100.00 36 0 0 133 168
1_30527 gi|3452552|dbj|AB001347.1| 100.00 34 0 0 6923 6956
1_30527 gi|3452552|dbj|AB001347.1| 100.00 34 0 0 2431 2464
1_30527 gi|3452552|dbj|AB001347.1| 100.00 34 0 0 2398 2431
1_30527 gi|3452552|dbj|AB001347.1| 100.00 33 0 0 2590 2622
1_30527 gi|3452552|dbj|AB001347.1| 100.00 33 0 0 2494 2526
1_30527 gi|3452552|dbj|AB001347.1| 97.22 36 1 0 2256 2291
1_30527 gi|3452552|dbj|AB001347.1| 100.00 33 0 0 2110 2142
1_30527 gi|3452552|dbj|AB001347.1| 100.00 32 0 0 1667 1698
1_30527 gi|3452552|dbj|AB001347.1| 97.06 34 1 0 4793 4826

```

1_30527	gi 3452552 dbj AB001347.1	100.00	31	0	0	2080	2110
1_30527	gi 3452552 dbj AB001347.1	100.00	30	0	0	6494	6523
1_30527	gi 3452552 dbj AB001347.1	100.00	30	0	0	3873	3902
1_30527	gi 3452552 dbj AB001347.1	100.00	30	0	0	1699	1728
1_30527	gi 3452552 dbj AB001347.1	100.00	30	0	0	1285	1314
1_30527	gi 3452552 dbj AB001347.1	96.88	32	1	0	5229	5260
1_30527	gi 3452552 dbj AB001347.1	100.00	29	0	0	523	551
1_30527	gi 3452552 dbj AB001347.1	100.00	28	0	0	3606	3633
1_30527	gi 3550974 dbj AB008551.1	92.00	300	0	12	193	480
1_30527	gi 3550974 dbj AB008551.1	81.78	516	40	43	3633	4115
1_30527	gi 3550974 dbj AB008551.1	86.09	381	9	24	4173	4530
1_30527	gi 3550974 dbj AB008551.1	84.07	427	9	24	4142	4530
1_30527	gi 3550974 dbj AB008551.1	99.48	193	1	0	1440	1632
1_30527	gi 3550974 dbj AB008551.1	100.00	144	0	0	1903	2046
1_30527	gi 3550974 dbj AB008551.1	98.65	148	2	0	2719	2866
1_30527	gi 3550974 dbj AB008551.1	95.92	147	0	2	5285	5431
1_30527	gi 3550974 dbj AB008551.1	100.00	121	0	0	7091	7211
1_30527	gi 3550974 dbj AB008551.1	93.75	144	0	2	673	807
1_30527	gi 3550974 dbj AB008551.1	93.15	146	1	1	3398	3543
1_30527	gi 3550974 dbj AB008551.1	86.87	198	7	11	2686	2866
1_30527	gi 3550974 dbj AB008551.1	93.33	135	0	6	6551	6676
1_30527	gi 3550974 dbj AB008551.1	100.00	91	0	0	4888	4978
1_30527	gi 3550974 dbj AB008551.1	98.89	90	1	0	6146	6235
1_30527	gi 3550974 dbj AB008551.1	98.90	91	0	1	4709	4798
1_30527	gi 3550974 dbj AB008551.1	86.76	136	0	7	5624	5741
1_30527	gi 3550974 dbj AB008551.1	81.54	195	8	19	5561	5741
1_30527	gi 3550974 dbj AB008551.1	98.70	77	0	1	1176	1252
1_30527	gi 3550974 dbj AB008551.1	91.09	101	0	4	5957	6057
1_30527	gi 3550974 dbj AB008551.1	84.06	138	12	10	6865	6997
1_30527	gi 3550974 dbj AB008551.1	90.62	96	0	1	1057	1143
1_30527	gi 3550974 dbj AB008551.1	84.25	127	5	9	5024	5135
1_30527	gi 3550974 dbj AB008551.1	87.50	96	0	4	2143	2238
1_30527	gi 3550974 dbj AB008551.1	98.18	55	1	0	6406	6460
1_30527	gi 3550974 dbj AB008551.1	88.10	84	4	5	4610	4688
1_30527	gi 3550974 dbj AB008551.1	91.55	71	3	3	2937	3006
1_30527	gi 3550974 dbj AB008551.1	82.35	119	10	10	6281	6392
1_30527	gi 3550974 dbj AB008551.1	83.19	113	6	9	5453	5560
1_30527	gi 3550974 dbj AB008551.1	100.00	49	0	0	1375	1423
1_30527	gi 3550974 dbj AB008551.1	87.36	87	2	2	961	1038
1_30527	gi 3550974 dbj AB008551.1	100.00	48	0	0	604	651
1_30527	gi 3550974 dbj AB008551.1	100.00	48	0	0	1	48
1_30527	gi 3550974 dbj AB008551.1	100.00	47	0	0	3050	3096
1_30527	gi 3550974 dbj AB008551.1	100.00	45	0	0	6731	6775
1_30527	gi 3550974 dbj AB008551.1	100.00	45	0	0	5831	5875
1_30527	gi 3550974 dbj AB008551.1	100.00	45	0	0	5156	5200
1_30527	gi 3550974 dbj AB008551.1	84.38	96	0	8	2287	2367
1_30527	gi 3550974 dbj AB008551.1	100.00	42	0	0	1733	1774
1_30527	gi 3550974 dbj AB008551.1	100.00	39	0	0	865	903
1_30527	gi 3550974 dbj AB008551.1	100.00	36	0	0	6074	6109
1_30527	gi 3550974 dbj AB008551.1	100.00	36	0	0	3291	3326
1_30527	gi 3550974 dbj AB008551.1	100.00	36	0	0	133	168
1_30527	gi 3550974 dbj AB008551.1	100.00	34	0	0	6923	6956
1_30527	gi 3550974 dbj AB008551.1	100.00	34	0	0	2431	2464
1_30527	gi 3550974 dbj AB008551.1	100.00	34	0	0	2398	2431
1_30527	gi 3550974 dbj AB008551.1	100.00	33	0	0	2590	2622
1_30527	gi 3550974 dbj AB008551.1	100.00	33	0	0	2494	2526
1_30527	gi 3550974 dbj AB008551.1	97.22	36	1	0	2256	2291
1_30527	gi 3550974 dbj AB008551.1	100.00	33	0	0	2110	2142
1_30527	gi 3550974 dbj AB008551.1	100.00	32	0	0	3961	3992
1_30527	gi 3550974 dbj AB008551.1	100.00	32	0	0	1667	1698

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=> S BETA SPECTRIN 3 AND RATTUS
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=> S SPECTRIN AND RATTUS
L2 2 SPECTRIN AND RATTUS

=> DUP REM L2
PROCESSING COMPLETED FOR L2
L3 2 DUP REM L2 (0 DUPLICATES REMOVED)

=> D 1

L3 ANSWER 1 OF 2 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2002:161955 BIOSIS
DN PREV200200161955
TI Synaptic scaffolding proteins in rat brain: Ankyrin repeats of the
multidomain Shank protein family interact with the cytoskeletal protein
alpha-fodrin.
AU Boeckers, Tobias M.; Mameza, Marie Germaine; Kreutz, Michael R.; Bockmann,
Juergen; Weise, Christoph; Buck, Fritz; Richter, Dietmar [Reprint author];
Gundelfinger, Eckart D. [Reprint author]; Kreienkamp, Hans-Juergen
CS Institut fuer Zellbiochemie und klinische Neurobiologie, Universitaet
Hamburg, Martinistraasse 52, 20246, Hamburg, Germany
richter@uke.uni-hamburg.de; gundelfinger@ifn-magdeburg.de
SO Journal of Biological Chemistry, (October 26, 2001) Vol. 276, No. 43, pp.
40104-40112. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 21 Feb 2002
Last Updated on STN: 26 Feb 2002

=> D 2

L3 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1998:472526 BIOSIS
DN PREV199800472526
TI Ancient large-scale genome duplications: Phylogenetic and linkage analyses
shed light on chordate genome evolution.
AU Pebusque, Marie-Josephe; Coulier, Francois; Birnbaum, Daniel [Reprint
author]; Pontarotti, Pierre

CS Inst Cancerologie d'Immunologie de Marseille, Univ. Mediterranee, INSERM U
119, 27 Bd Lei Roure 13009 Marseille, France
SO Molecular Biology and Evolution, (Sept., 1998) Vol. 15, No. 9, pp.
1145-1159. print.
CODEN: MBEVEO. ISSN: 0737-4038.
DT Article
LA English
ED Entered STN: 5 Nov 1998
Last Updated on STN: 5 Nov 1998

=> S GTRAP41 AND RATTUS
L4 0 GTRAP41 AND RATTUS

=> S GTRAP* AND RATTUS
L5 0 GTRAP* AND RATTUS

=> S SPNB3 AND RATTUS
L6 0 SPNB3 AND RATTUS

=> S SPN* AND RATTUS
L7 0 SPN* AND RATTUS

=> LOGOFF HOLD
COST IN U.S. DOLLARS
FULL ESTIMATED COST

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